

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 01:09:51 ; Search time 23.6667 Seconds
(without alignments)
19.615 Million cell updates/sec

Title: US-09-712-819D-13
Perfect score: 31
Sequence: 1 LTLKLSR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 58200

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	18	58.1	5	3	US-08-981-122-65
2	18	58.1	7	3	US-09-173-941-72
3	18	58.1	7	4	US-09-423-468A-6
4	18	58.1	7	4	US-09-494-190-72
5	17	54.8	6	2	US-08-637-759B-219
6	17	54.8	6	3	US-08-871-355A-219
7	17	54.8	6	3	US-09-201-945-219
8	17	54.8	7	2	US-08-968-676-70
9	16	51.6	6	4	US-09-428-082B-532
10	16	51.6	7	1	US-08-239-854-1
11	16	51.6	7	1	US-08-239-854-2
12	16	51.6	7	1	US-08-346-333-24
13	16	51.6	7	2	US-08-968-676-117
14	16	51.6	7	2	US-08-968-676-121
15	16	51.6	7	5	PCT-US91-07506-24
16	15	48.4	6	1	US-08-066-325-144
17	15	48.4	6	2	US-08-177-109A-42
18	15	48.4	6	2	US-08-687-706-42
19	15	48.4	6	2	US-08-482-228-180
20	15	48.4	6	3	US-08-482-528-180
21	15	48.4	6	4	US-09-383-062-35
22	15	48.4	6	5	PCT-US95-08354A-9
23	15	48.4	6	6	5342922-6
24	15	48.4	7	2	US-08-968-676-4
25	15	48.4	7	2	US-08-968-676-23
26	15	48.4	7	2	US-08-545-745-4
27	15	48.4	7	3	US-08-654-623-69

28	15	48.4	7	3	US-09-173-941-62	Sequence 62, Appl
29	15	48.4	7	3	US-09-173-941-66	Sequence 66, Appl
30	15	48.4	7	3	US-09-173-941-67	Sequence 67, Appl
31	15	48.4	7	3	US-09-173-941-68	Sequence 68, Appl
32	15	48.4	7	3	US-09-139-802-76	Sequence 76, Appl
33	15	48.4	7	3	US-09-268-992-78	Sequence 78, Appl
34	15	48.4	7	3	US-09-657-474-78	Sequence 78, Appl
35	15	48.4	7	4	US-09-396-813-4	Sequence 4, Appli
36	15	48.4	7	4	US-09-659-786-76	Sequence 76, Appl
37	15	48.4	7	4	US-08-926-914-76	Sequence 76, Appl
38	15	48.4	7	4	US-09-494-190-62	Sequence 62, Appl
39	15	48.4	7	4	US-09-494-190-66	Sequence 66, Appl
40	15	48.4	7	4	US-09-494-190-67	Sequence 67, Appl
41	15	48.4	7	4	US-09-494-190-68	Sequence 68, Appl
42	15	48.4	7	4	US-09-771-415-12	Sequence 12, Appl
43	14	45.2	4	1	US-08-305-871A-17	Sequence 17, Appl
44	14	45.2	4	4	US-08-788-822A-1	Sequence 1, Appli
45	14	45.2	5	1	US-08-409-199-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-981-122-65
; Sequence 65, Application US/08981122B
; Patent No. 6127339
; GENERAL INFORMATION:
; APPLICANT: Hatanaka, Yoshihiro
; APPLICANT: Aritomi, Masaharu
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/08/981,122B
; CURRENT FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: JP 7-176904
; PRIOR FILING DATE: 1995-06-21
; PRIOR APPLICATION NUMBER: PCT/JP96/01734
; PRIOR FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of a peptide synthesized in Comparative Example 1 from Patent No. 6127339
; OTHER INFORMATION: L-form F-moc amino acids by solid phase method using a
; OTHER INFORMATION: multi-peptide synthesizing system (RAMPS)
US-08-981-122-65

Query Match 58.1%; Score 18; DB 3; Length 5;
Best Local Similarity 60.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LTLKL 5
Db 1 LTKM 5

RESULT 2
US-09-173-941-72
; Sequence 72, Application US/09173941
; Patent No. 6140081
; GENERAL INFORMATION:
; APPLICANT: BARBAS, Carlos F.
; TITLE OF INVENTION: ZINC FINGER BINDING DOMAINS FOR GNN
; FILE REFERENCE: NOV0081S
; CURRENT APPLICATION NUMBER: US/09/173,941
; CURRENT FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72

US-09-494-190-72

Query Match 58.1%; Score 18; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KLSR 7
Db 4 KLSR 7

RESULT 5

US-08-637-759B-219
; Sequence 219, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,759B
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 219:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-637-759B-219

Query Match 54.8%; Score 17; DB 2; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LKLSR 7
Db 2 LKLMR 6

RESULT 6

US-08-871-355A-219
; Sequence 219, Application US/08871355A
; Patent No. 6015669
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes

US-09-494-190-72

Query Match 58.1%; Score 18; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KLSR 7
Db 4 KLSR 7

RESULT 5

US-08-637-759B-219
; Sequence 219, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,759B
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 219:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-637-759B-219

Query Match 54.8%; Score 17; DB 2; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LKLSR 7
Db 2 LKLMR 6

RESULT 6

US-08-871-355A-219
; Sequence 219, Application US/08871355A
; Patent No. 6015669
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes


```
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
Db 1 LRLKLPK 7

RESULT 9
US-09-428-082B-532
Sequence 532, Application US/09428082B
Patent No. 6660843
GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-FA
APPLICANT: CHEETHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/09/428,082B
CURRENT FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PatentIn version 3.1
SEQ ID NO 532
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: ANTIPATHOGENIC PEPTIDE
US-09-428-082B-532

Query Match 51.6%; Score 16; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTLKL 5
Db 2 LILKL 6

RESULT 10
US-08-239-854-1
Sequence 1, Application US/08239854
Patent No. 5624900
GENERAL INFORMATION:
APPLICANT: Suda, Tatsuo
APPLICANT: Abe, Etsuko
APPLICANT: Tanihara, Masao
APPLICANT: Fujiwara, Chie
TITLE OF INVENTION: Peptide or Its Salts
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/239,854
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/752,426
FILING DATE:
APPLICATION NUMBER: JP 233,571/90
FILING DATE: 03-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 320,000/90
FILING DATE: 24-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 324,956/90
FILING DATE: 26-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5624900man F.
REGISTRATION NUMBER: 24,618

Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LTLKLS 6
Db 2 LRLKIS 7

RESULT 11
US-08-239-854-2
Sequence 2, Application US/08239854
Patent No. 5624900
GENERAL INFORMATION:
APPLICANT: Suda, Tatsuo
APPLICANT: Abe, Etsuko
APPLICANT: Tanihara, Masao
APPLICANT: Fujiwara, Chie
TITLE OF INVENTION: Peptide or Its Salts
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/239,854
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/752,426
FILING DATE:
APPLICATION NUMBER: JP 233,571/90
FILING DATE: 03-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 320,000/90
FILING DATE: 24-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 324,956/90
FILING DATE: 26-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5624900man F.
REGISTRATION NUMBER: 24,618

FILING DATE: 03-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 320,000/90
FILING DATE: 26-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5624900man F.
REGISTRATION NUMBER: 24,618

Query Match 51.6%; Score 16; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTLKLS 6
Db 2 LRLKIS 7

US-08-239-854-1
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/ REFERENCE/DOCKET NUMBER: 363-279-0
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703)521-4500
/ TELEFAX: (703)486-2347
/ TELEX: 248855 OPAT UR
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 7 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-239-854-2

Query Match 51.6%; Score 16; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTLKLS 6
| : |
Db 2 LQIKIS 7

RESULT 12
US-08-346-333-24
/ Sequence 24, Application US/08346333
/ Patent No. 5677153
/ GENERAL INFORMATION:
/ APPLICANT: Botstein, David
/ APPLICANT: Palzkill, Timothy
/ TITLE OF INVENTION: Methods for modifying DNA and for
/ TITLE OF INVENTION: detecting effects of such modification on interaction of
/ TITLE OF INVENTION: encoded modified polypeptides with target substrates.
/ NUMBER OF SEQUENCES: 86
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Richard F. Trecartin
/ STREET: 4 Embarcadero Center, Suite 3400
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111

/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/346,333
/ FILING DATE:

/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/039,501
/ FILING DATE:
/ APPLICATION NUMBER: US 07/602,158
/ FILING DATE: 22-OCT-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Trecartin, Richard F.
/ REGISTRATION NUMBER: 31,801
/ REFERENCE/DOCKET NUMBER: A-53469/RPT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 781-1989
/ TELEFAX: (415) 398-3249
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 7 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-346-333-24

Query Match 51.6%; Score 16; DB 1; Length 7;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKL 5
| : |
Db 2 TLKI 5

RESULT 13
US-08-968-676-117
/ Sequence 117, Application US/08968676
/ Patent No. 5919639
/ GENERAL INFORMATION:
/ APPLICANT: Humphreys, Robert E
/ APPLICANT: Adams, Sharlene
/ APPLICANT: Xu, Minzhen
/ TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
/ NUMBER OF SEQUENCES: 165
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Kevin M. Farrell, P.C.
/ STREET: P.O. Box 999
/ CITY: York Harbor
/ STATE: ME
/ COUNTRY: USA
/ ZIP: 03911
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/968,676
/ FILING DATE:
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Farrell, Kevin M
/ REGISTRATION NUMBER: 35,505
/ REFERENCE/DOCKET NUMBER: REH-9601
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (207) 363-0558
/ TELEFAX: (207) 363-0528
/ INFORMATION FOR SEQ ID NO: 117:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 7 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: Modified-site
/ OTHER INFORMATION: /note= "The Xaa at position 2 is the D-
/ OTHER INFORMATION: amino acid of Arg."
US-08-968-676-117

Query Match 51.6%; Score 16; DB 2; Length 7;
Best Local Similarity 42.9%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
| : | :
Db 1 LXMKLPK 7

RESULT 14
US-08-968-676-121
/ Sequence 121, Application US/08968676
/ Patent No. 5919639
/ GENERAL INFORMATION:
/ APPLICANT: Humphreys, Robert E
/ APPLICANT: Adams, Sharlene
/ APPLICANT: Xu, Minzhen
/ TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
/ NUMBER OF SEQUENCES: 165
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Kevin M. Farrell, P.C.

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OM protein - protein search, using sw model

Run on: November 4, 2004, 01:09:31 ; Search time 18.3333 Seconds
(without alignments)
36.737 Million cell updates/sec

Title: US-09-712-819D-13
Perfect score: 31
Sequence: 1 LTKLSR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	13	41.9	7	2 S19630	ribosomal protein
2	11	35.5	3	3 T13892	cytochrome-c oxida
3	11	35.5	4	2 T46627	hypothetical prote
4	11	35.5	5	2 E42364	flagellar protein
5	11	35.5	6	2 I49424	cytotoxic T-lympho
6	11	35.5	7	2 JN0859	peptidyl-dipeptida
7	11	35.5	7	2 A28709	phosphonoacetaldeh
8	11	35.5	7	2 E48394	glycoprotein compo
9	11	35.5	7	2 I48086	DNA topoisomerase
10	11	35.5	7	2 B48394	major fat-globule
11	10	32.3	4	2 I40505	hypothetical prote
12	10	32.3	5	2 T14910	hypothetical prote
13	10	32.3	6	2 I48126	alpha-tubulin - Ch
14	10	32.3	6	2 B33932	IG mu chain D regi
15	10	32.3	7	2 PN0649	pululanase (EC 3.
16	10	32.3	7	2 A30812	sex pheromone cCf1
17	10	32.3	7	2 A28340	myomodulin - Calif
18	10	32.3	7	2 ECMUCR	catch-relaxing pep
19	9	29.0	5	2 C41225	copper resistance
20	9	29.0	5	2 PT0525	T-cell receptor be
21	9	29.0	5	2 PT0577	T-cell receptor be
22	9	29.0	5	2 PT0700	T-cell receptor be
23	9	29.0	5	2 S69237	surface protein te
24	9	29.0	5	2 PT0565	T-cell receptor be
25	9	29.0	6	2 B34835	dnaA protein - Pse
26	9	29.0	6	2 A43766	28K ubiquitin-immu
27	9	29.0	6	2 I65546	MHC H2-L antigen -
28	9	29.0	6	2 PT0518	T-cell receptor be
29	9	29.0	6	2 PT0662	T-cell receptor be

30	9	29.0	7	2 S25266	pile protein - Esc
31	9	29.0	7	2 PN0150	omega-gliadine 1'
32	9	29.0	7	2 S78024	ribosomal protein
33	9	29.0	7	2 E30608	Ig kappa chain V-1
34	9	29.0	7	2 PT0671	T-cell receptor be
35	9	29.0	7	2 PX0008	glucuronosyltransf
36	9	29.0	7	2 S66442	glutathione S-tran
37	9	29.0	7	2 S09066	globulin IV alpha
38	9	29.0	7	2 A15398	choline oxidase (E
39	8	25.8	4	2 I61883	protamine P1 - ora
40	8	25.8	4	2 I37013	protamine P1 - Cer
41	8	25.8	4	2 I84439	protamine P1 - sav
42	8	25.8	5	2 I39964	ribosomal protein
43	8	25.8	5	2 I39966	ribosomal protein
44	8	25.8	5	2 I39965	ribosomal protein
45	8	25.8	5	2 G44817	27.5 kda structura

ALIGNMENTS

RESULT 1
S19630
ribosomal protein L30 - Streptomyces griseus (fragment)
C;Species: Streptomyces griseus
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 06-Jun-1997
C;Accession: S19630
R;Ochi, K.
Int. J. Syst. Bacteriol. 42, 144-150, 1992
A;Title: Electrophoretic heterogeneity of ribosomal protein AT-L30 among actinomycete g
A;Reference number: S19630; MUID:92144363; PMID:1736962
A;Accession: S19630
A;Molecule type: protein
A;Residues: 1-7 <OCH>
A;Experimental source: strain IFO 13189
C;Superfamily: Escherichia coli ribosomal protein L30
C;Keywords: protein biosynthesis; ribosome

Query Match 41.9%; Score 13; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LKLSR 7
Db 3 LKITQ 7

RESULT 2
T13892

cytochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrion (frag
C;Species: mitochondrion Lampetra fluviatilis (river lamprey)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: T13892
R;Delarbre, C.; Barriol, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol. 14, 807-813, 1997
A;Title: The main features of the craniate mitochondrial DNA between the ND1 and the COI
A;Reference number: Z17775; MUID:97398704; PMID:9254918
A;Accession: T13892
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-3
A;Cross-references: EMBL:Y09528; NID:G2340016; PIDN:CAA70721.1; PID:G4379123
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match 35.5%; Score 11; DB 3; Length 3;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LTL 3
:|||

Db	1 MTL 3	Matches	2;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
RESULT 3											
T46627											
hypothetical protein c4 - loblolly pine											
C;Species: Pinus taeda (loblolly pine)											
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000											
C;Accession: T46627											
R;Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.											
submitted to the EMBL Data Library, July 1995											
A;Description: Cloning of a chitinase homolog which lacks chitin binding sites and is do											
A;Reference number: Z23105											
A;Accession: T46627											
A;Status: preliminary; translated from GB/EMBL/DBJ											
A;Molecule type: mRNA											
A;Residues: 1-4 <CHA>											
A;Cross-references: EMBL:U31309; NID:g974285; PID:g974292											
A;Experimental source: strain s6PT2xs6PT3; 8 month seedlings											
Query Match											
Best Local Similarity											
Matches											
QY	3 LKL 5	35.5%;	Score 11;	DB 2;	Length 4;						
	:										
Db	1 MKL 3	66.7%;	Pred. No. 2.8e+05;								
RESULT 4											
E42364											
flagellar protein flir - Salmonella typhimurium (fragment)											
C;Species: Salmonella typhimurium											
C;Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 09-Jul-2004											
C;Accession: E42364											
R;Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.											
J. Bacteriol. 173, 3564-3572, 1991											
A;Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and seq											
A;Reference number: A42364; MUID:91258342; PMID:1646201											
A;Accession: E42364											
A;Status: preliminary											
A;Molecule type: DNA											
A;Residues: 1-5 <VOG>											
A;Cross-references: UNIPROT:P26416; GB:M62408											
Query Match											
Best Local Similarity											
Matches											
QY	1 LTL 3	35.5%;	Score 11;	DB 2;	Length 5;						
	:										
Db	2 ITL 4	66.7%;	Pred. No. 2.8e+05;								
RESULT 5											
I49424											
cytotoxic T-lymphocyte proteinase 3 (EC 3.4.21.-) - western wild mouse (fragment)											
C;Species: Mus spretus (western wild mouse)											
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999											
C;Accession: I49424											
R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H											
Mamm. Genome 5, 349-355, 1994											
A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.											
A;Reference number: I48934; MUID:94319082; PMID:8043949											
A;Accession: I49424											
A;Status: preliminary; translated from GB/EMBL/DBJ											
A;Molecule type: DNA											
A;Residues: 1-6 <RES>											
A;Cross-references: EMBL:U05745; NID:g497084; PIDN:AAB60481.1; PID:g642831											
C;Keywords: hydrolase; serine proteinase											
Query Match											
Best Local Similarity											
Matches											
QY	3 LXL 5	35.5%;	Score 11;	DB 2;	Length 7;						
	:										
Db	1 LXL 3	66.7%;	Pred. No. 2.8e+05;								
RESULT 6											
JN0859											
peptidyl-dipeptidase A inhibitory peptide C105 - striped bonito											
C;Species: Sarda orientalis (striped bonito)											
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999											
C;Accession: JN0859											
R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.											
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993											
A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory p											
A;Reference number: JN0859; MUID:94080036; PMID:7764272											
A;Accession: JN0859											
A;Molecule type: protein											
A;Residues: 1-7 <MAT>											
A;Experimental source: intestine											
C;Comment: The carboxyl-terminus is essential for the protein's expression of angiotens											
C;Superfamily: bradykinin-potentiating peptide											
C;Keywords: angiotensin-converting enzyme inhibitor											
Query Match											
Best Local Similarity											
Matches											
QY	4 KLSR 7	35.5%;	Score 11;	DB 2;	Length 7;						
	:										
Db	4 KLEK 7	50.0%;	Pred. No. 2.8e+05;								
RESULT 7											
A28709											
phosphonoacetaldehyde hydrolase - Bacillus cereus (fragment)											
C;Species: Bacillus cereus											
C;Date: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 30-Sep-1993											
C;Accession: A28709											
R;Olson, D.B.; Hepburn, T.W.; Moos, M.; Mariano, P.S.; Dunaway-Mariano, D.											
Biochemistry 27, 2229-2234, 1988											
A;Title: Investigation of the Bacillus cereus phosphonoacetaldehyde hydrolase. Evidence											
due.											
A;Reference number: A28709; MUID:88241058; PMID:3132206											
A;Accession: A28709											
A;Status: preliminary											
A;Molecule type: protein											
A;Residues: 1-7 <OLS>											
Query Match											
Best Local Similarity											
Matches											
QY	3 LXL 5	35.5%;	Score 11;	DB 2;	Length 7;						
	:										
Db	1 LXL 3	66.7%;	Pred. No. 2.8e+05;								
RESULT 8											
E48394											
glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (
C;Species: Bos primigenius taurus (cattle)											
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997											
C;Accession: E48394											
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.											
Biochem. Mol. Biol. Int. 29, 545-554, 1993											
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-p											
II-like sequences.											
A;Reference number: A48394; MUID:93250576; PMID:8485470											
A;Accession: E48394											
A;Status: preliminary											
A;Molecule type: protein											

A;Residues: 1-7 <MAT>

A;Experimental source: milk

A;Note: sequence extracted from NCBI backbone (NCBIP:131450)

C;Keywords: glycoprotein

Query Match 35.5%; Score 11; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 KLSR 7

:|:|

Db 4 ELAR 7

RESULT 9

I48086

DNA topoisomerase II alpha - Chinese hamster (fragment)

C;Species: Cricetulus griseus (Chinese hamster)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C;Accession: I48086

R;Ng, S.W.; Eder, J.P.; Schnipper, L.E.; Chan, V.T.W.

J. Biol. Chem. 270, 25850-25858, 1995

A;Title: Molecular cloning and characterization of the promoter for the Chinese hamster

A;Reference number: I48086; MUID:96029684; PMID:7592770

A;Accession: I48086

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-7 <RES>

A;Cross-references: EMBL:U34196; NID:g1041231; PIDN:AAC52315.1; PID:g1041232

Query Match

Best Local Similarity 35.5%; Score 11; DB 2; Length 7;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LKLS 6

:|:|

Db 1 MELS 4

RESULT 10

B48394

major fat-globule membrane protein GP 55 - guinea pig (fragment)

C;Species: Cavia porcellus (guinea pig)

C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995

C;Accession: B48394

R;Mather, I.H.; Banghart, L.R.; Lane, W.S.

Biochem. Mol. Biol. Int. 29, 545-554, 1993

A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig II-like sequences.

A;Reference number: A48394; MUID:93250576; PMID:8485470

A;Accession: B48394

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <MAT>

A;Experimental source: milk

A;Note: sequence extracted from NCBI backbone (NCBIP:131444)

Query Match

Best Local Similarity 35.5%; Score 11; DB 2; Length 7;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 KLSR 7

:|:|

Db 4 ELAR 7

RESULT 11

I40505

hypothetical protein 3 (4 aa) - Bacillus stearothermophilus

C;Species: Bacillus stearothermophilus

C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Oct-1999

C;Accession: I40505

R;Waye, M.M.; Winter, G.

Eur. J. Biochem. 158, 505-510, 1986

A;Title: A transcription terminator in the 5' non-coding region of the tyrosyl tRNA synthetase gene of *Escherichia coli*

A;Reference number: I40503; MUID:86274732; PMID:3525162

A;Accession: I40505

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-4 <RES>

A;Cross-references: EMBL:X04193; NID:g40233; PIDN:CAA27783.1; PID:g580944

Query Match

Best Local Similarity 32.3%; Score 10; DB 2; Length 4;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LSR 7

:|:|

Db 2 LSK 4

RESULT 12

T14910

hypothetical protein - parsley

C;Species: Petroselinum crispum (parsley)

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000

C;Accession: T14910

R;Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.

Mol. Gen. Genet. 257, 595-605, 1998

A;Title: CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis of

A;Reference number: Z18261; MUID:98265918; PMID:9604882

A;Accession: T14910

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-5 <KIR>

A;Cross-references: EMBL:Y10810; NID:g3336904; PIDN:CAA71769.1; PID:g3336905

A;Experimental source: ssp. Hamburger Schnitt

Query Match

Best Local Similarity 32.3%; Score 10; DB 2; Length 5;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LSR 7

:|:|

Db 2 VSR 4

RESULT 13

I48126

alpha-tubulin - Chinese hamster (fragment)

C;Species: Cricetulus griseus (Chinese hamster)

C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999

C;Accession: I48126

R;Elliot, B.M.; Sarangi, F.; Henderson, G.; Ling, V.

Can. J. Biochem. Cell Biol. 63, 511-518, 1985

A;Title: Cloning of 11 alpha-tubulin gene sequences from the genome of Chinese hamster

A;Reference number: I48126; MUID:86001952; PMID:2931165

A;Accession: I48126

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-6 <RES>

A;Cross-references: GB:M25895; NID:g341417; PIDN:AAA74493.1; PID:g516601

C;Genetics:

A;Introns: 3/3

Query Match

Best Local Similarity 32.3%; Score 10; DB 2; Length 6;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KLS 6

:|:|

Db 2 KLA 4

RESULT 14

B33932

Ig mu chain D region (D23) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 16-Aug-1996
C;Accession: B33932
R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
A;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-l
A;Reference number: A33932; MUID:89282823; PMID:2499887
A;Accession: B33932
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-6 <BAC>
A;Cross-references: GB:M27107
C;Keywords: immunoglobulin

Query Match 32.3%; Score 10; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LKL 5
|:|
Db 3 LRL 5

RESULT 15
PN0649
pullulanase (EC 3.2.1.41) - Bacillus sp. (strain S-1) (fragment)
C;Species: Bacillus sp.
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 03-Jun-2002
C;Accession: PN0649
R;Kim, C.H.; Choi, H.I.; Lee, D.S.
Biosci. Biotechnol. Biochem. 57, 1632-1637, 1993
A;Title: Purification and biochemical properties of an alkaline pullulanase from alkalop
A;Reference number: PN0649; MUID:94080025; PMID:7764261
A;Accession: PN0649
A;Molecule type: protein
A;Residues: 1-7 <KIM>
C;Comment: This enzyme is used together with glucoamylase to improve the efficiency of st
nent in high maltose syrups.
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 32.3%; Score 10; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LKLS 6
|:|
Db 2 LNMS 5

Search completed: November 4, 2004, 01:24:17
Job time : 18.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:55:00 ; Search time 99.6667 Seconds
(without alignments)
40.411 Million cell updates/sec

Title: US-09-712-819D-13
Perfect score: 31
Sequence: 1 LTKLSR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 segs, 575374646 residues

Total number of hits satisfying chosen parameters: 167

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	13	41.9	7	2 Q95945	Q95945 saccharomyc
2	11	35.5	6	2 P82181	P82181 spinacia ol
3	11	35.5	6	2 P82182	P82182 spinacia ol
4	11	35.5	7	2 Q8GL00	Q8GL00 borrelia bu
5	11	35.5	7	2 Q8JE81	Q8JE81 human immun
6	10	32.3	6	2 P82541	P82541 spinacia ol
7	10	32.3	7	1 CARP_MYTED	P10420 mytilus edu
8	10	32.3	7	1 CCF1_ENTFA	P20104 enterococcu
9	10	32.3	7	2 P83530	P83530 lactobacill
10	9	29.0	4	2 Q08433	Q08433 rattus sp.
11	9	29.0	5	1 FARP_CHICK	P83308 gallus gall
12	9	29.0	7	1 CHO_X_ALCSP	P16101 alcaligenes
13	9	29.0	7	1 UC24_MAIZE	P80630 zea mays (m
14	9	29.0	7	2 Q15897	Q15897 homo sapien
15	9	29.0	7	2 P93233	P93233 lycopersico
16	9	29.0	7	2 O07354	O07354 synechococc
17	9	29.0	7	2 Q8GL04	Q8GL04 borrelia bu
18	9	29.0	7	2 Q8GL12	Q8GL12 borrelia bu
19	9	29.0	7	2 Q8K3H6	Q8K3H6 rattus norv
20	9	29.0	7	2 Q66205	Q66205 transmissib
21	8	25.8	5	1 E104_LITRU	P82100 litorea rub
22	8	25.8	7	1 FAR5_HIRME	P42564 hirudo medi
23	8	25.8	7	1 GFRP_MOUSE	P99025 mus musculu
24	8	25.8	7	2 Q9C5B3	Q9C5B3 arabidopsis
25	8	25.8	7	2 O34028	O34028 sphingomona
26	8	25.8	7	2 P70804	P70804 azotobacter
27	8	25.8	7	2 Q66113	Q66113 cherry leaf
28	8	25.8	7	2 Q9YIQ9	Q9YIQ9 human adeno
29	8	25.8	7	2 Q9YI90	Q9YI90 human adeno
30	8	25.8	7	2 Q9YVE3	Q9YVE3 human adeno
31	8	25.8	7	2 O42564	O42564 fugu rubrip

32	7	22.6	3	1 LUXE_VIBFI	P24272 vibrio fisc
33	7	22.6	5	1 BIOA_CITFR	P13071 citrobacter
34	7	22.6	5	1 UFO1_MOUSE	P38639 mus musculu
35	7	22.6	5	2 P83073	P83073 bacillus ce
36	7	22.6	6	1 ACPH_RABIT	P25154 oryctolagus
37	7	22.6	6	1 UN06_CLOPA	P81351 clostridium
38	7	22.6	6	1 VPI9_HHV1K	P23210 human herpe
39	7	22.6	7	1 ALL7_CYPDO	P82158 cydia pomon
40	7	22.6	7	1 WWA1_ACHFU	P35919 achatina fu
41	7	22.6	7	1 WWA2_ACHFU	P35920 achatina fu
42	7	22.6	7	1 WWA3_ACHFU	P35921 achatina fu
43	7	22.6	7	2 Q28742	Q28742 oryctolagus
44	7	22.6	7	2 P92210	P92210 agropyron c
45	7	22.6	7	2 P92214	P92214 amblyopyrum

ALIGNMENTS

RESULT 1

Q95945
ID Q95945 PRELIMINARY; PRT; 7 AA.
AC Q95945;
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Inside intron 5 (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D273-10B;
RX MEDLINE=81069885; PubMed=6254986;
RA Bonitz S.G.; Coruzzi G.; Thalenfeld B.; Tzagoloff A.; Macino G.;
RT "Assembly of the mitochondrial membrane system: Structure and
RT nucleotide sequence of the gene coding for subunit 1 of yeast
RT cytochrome oxidase.";
RL J. Biol. Chem. 255:11927-11941(1980).
DR EMBL; V00694; CAA24066.1; -
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;

Query Match 41.9%; Score 13; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KLS 6
Db 5 KLS 7

RESULT 2

P82181
ID P82181 PRELIMINARY; PRT; 6 AA.
AC P82181;
DT 01-JUN-2000 (Tremblrel. 14, Created)
DT 01-JUN-2000 (Tremblrel. 14, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Chloroplast 50S ribosomal protein l10 beta (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. ALWARO; TISSUE=Leaf;
RX MEDLINE=20435798; PubMed=10874046;


```
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 kDa.
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0019843; F:rRNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro; IPR002363; Ribosomal_L10eub.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KW Chloroplast; Ribosomal protein; rRNA-binding.
FT NON TER 6
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 35.5%; Score 11; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LSR 7
Db 2 ISR 4

RESULT 3
P82182 ID P82182 PRELIMINARY; PRT; 6 AA.
AC P82182;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 gamma (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. ALVARO; TISSUE=Leaf;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 kDa.
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0019843; F:rRNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro; IPR002363; Ribosomal_L10eub.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KW Chloroplast; Ribosomal protein; rRNA-binding.
FT NON TER 6
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 35.5%; Score 11; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LSR 7
Db 2 ISR 4

RESULT 4
Q8GL00 ID Q8GL00 PRELIMINARY; PRT; 7 AA.
AC Q8GL00;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PF-50 protein (Fragment).
GN Name=PF-50;
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid group cp32-13.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CA15;
RX MEDLINE=22610300; PubMed=12724373;
RA Miller J.C., Stevenson B.;
RT "Immunological and genetic characterization of Borrelia burgdorferi
RT Bapa and EppA proteins.";
RL Microbiology 149:1113-1125(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CA15;
RX MEDLINE=22990544; PubMed=14629041;
RA Stevenson B., Miller J.C.;
RT "Intra- and interbacterial genetic exchange of Lyme disease spirochete
RT erp genes generates sequence identity amidst diversity.";
RL J. Mol. Evol. 57:309-324(2003).
DR EMBL; AY142106; AAN17857.1; -.
KW Plasmid.
FT NON TER 1
SQ SEQUENCE 7 AA; 928 MW; 6337233050437350 CRC64;

Query Match 35.5%; Score 11; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LKL 5
Db 4 IKL 6

RESULT 5
Q8JE81 ID Q8JE81 PRELIMINARY; PRT; 7 AA.
AC Q8JE81;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Truncated pol protein (Fragment).
GN Name-pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22056123; PubMed=12060770;
RA Beerewinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,
RA Hoffmann D., Korn K., Selbig J.;
RT "Diversity and complexity of HIV-1 drug resistance: a bioinformatics
RT approach to predicting phenotype from genotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).
DR EMBL; AF347267; AAK32344.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 885 MW; 76C37731A046C700 CRC64;

Query Match 35.5%; Score 11; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTL 3
Db 3 ITL 5
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RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 kDa.
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0019843; F:rRNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro; IPR002363; Ribosomal_L10eub.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KW Chloroplast; Ribosomal protein; rRNA-binding.
FT NON TER 6
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 35.5%; Score 11; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LSR 7
Db 2 ISR 4

RESULT 3
P82182 ID P82182 PRELIMINARY; PRT; 6 AA.
AC P82182;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 gamma (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. ALVARO; TISSUE=Leaf;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 kDa.
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0019843; F:rRNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro; IPR002363; Ribosomal_L10eub.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KW Chloroplast; Ribosomal protein; rRNA-binding.
FT NON TER 6
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 35.5%; Score 11; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LSR 7
Db 2 ISR 4

RESULT 4
Q8GL00 ID Q8GL00 PRELIMINARY; PRT; 7 AA.
AC Q8GL00;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PF-50 protein (Fragment).
GN Name=PF-50;
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid group cp32-13.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CA15;
RX MEDLINE=22610300; PubMed=12724373;
RA Miller J.C., Stevenson B.;
RT "Immunological and genetic characterization of Borrelia burgdorferi
RT Bapa and EppA proteins.";
RL Microbiology 149:1113-1125(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CA15;
RX MEDLINE=22990544; PubMed=14629041;
RA Stevenson B., Miller J.C.;
RT "Intra- and interbacterial genetic exchange of Lyme disease spirochete
RT erp genes generates sequence identity amidst diversity.";
RL J. Mol. Evol. 57:309-324(2003).
DR EMBL; AY142106; AAN17857.1; -.
KW Plasmid.
FT NON TER 1
SQ SEQUENCE 7 AA; 928 MW; 6337233050437350 CRC64;

Query Match 35.5%; Score 11; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LKL 5
Db 4 IKL 6

RESULT 5
Q8JE81 ID Q8JE81 PRELIMINARY; PRT; 7 AA.
AC Q8JE81;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Truncated pol protein (Fragment).
GN Name-pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22056123; PubMed=12060770;
RA Beerewinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,
RA Hoffmann D., Korn K., Selbig J.;
RT "Diversity and complexity of HIV-1 drug resistance: a bioinformatics
RT approach to predicting phenotype from genotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).
DR EMBL; AF347267; AAK32344.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 885 MW; 76C37731A046C700 CRC64;

Query Match 35.5%; Score 11; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTL 3
Db 3 ITL 5
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RESULT 6
P82541      PRELIMINARY;      PRT;      6 AA.
AC P82541;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chloroplast 30S ribosomal protein S19 beta (Fragment).
OS Spinacia oleracea (Spinach).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC STRAIN=cv. ALWARO; TISSUE=Leaf;
RX MEDLINE=20435797; PubMed=10874039;
RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the small subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 37:28455-28465(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
CC -!- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
CC -!- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA
CC FORM IS THE MINOR BASIC FORM.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 kDa.
CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
DR GO: GO:0009507; C:chloroplast; IEA.
DR GO: GO:0019843; F:rRNA binding; IEA.
DR GO: GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro; IPR002222; Ribosomal S19.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Chloroplast; Ribosomal protein; rRNA-binding.
FT NON TER
SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;

Query Match 32.3%; Score 10; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLK 4
Db 3 SLK 5

RESULT 7
CARP_MYTED      STANDARD;      PRT;      7 AA.
AC P10420;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Catch-relaxing peptide (CARP).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RX MEDLINE=88052022; PubMed=3676797;
RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
RA Muneoka Y.;
RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";
RL Brain Res. 422:374-376(1987).
CC -!- FUNCTION: This peptide exhibits both potentiating (contraction)
CC and inhibitory (relaxation) effects on the anterior byssus
CC retractor muscle.
DR PIR; A29342; ECMUCR.
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KW Amidation; Direct protein sequencing; Hormone.
FT MOD RES 7 Leucine amide.
SQ SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;

Query Match 32.3%; Score 10; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LKL 5
Db 5 LRL 7

RESULT 8
CCFL_ENTFA      STANDARD;      PRT;      7 AA.
AC P20104;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sex pheromone cCF10.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=89008313; PubMed=3139658;
RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
RA Adsit J.C., Dunny G.M., Suzuki A.;
RT "Structure of cCF10, a peptide sex pheromone which induces conjugative
RT transfer of the Streptococcus faecalis tetracycline resistance
RT plasmid, pCF10.";
RL J. Biol. Chem. 263:14574-14578(1988).
CC -!- FUNCTION: cCF10 is involved in the conjugative transfer of the
CC hemolysin plasmid pCF10.
DR PIR; A30812; A30812.
KW Direct protein sequencing; Pheromone.
SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;

Query Match 32.3%; Score 10; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTL 3
Db 2 VTL 4

RESULT 9
P83530      PRELIMINARY;      PRT;      7 AA.
AC P83530;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 20451;
RX PubMed=12112860;
RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
RT "High pressure effects step-wise altered protein expression in
RT Lactobacillus sanfranciscensis.";
RL Proteomics 2:765-774(2002).
CC -!- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
CC protein is: 15 kDa.
FT NON TER 1
FT NON TER 7
SQ SEQUENCE 7 AA; 790 MW; 6AAB02CAA731B2A0 CRC64;
```

SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 29.0%; Score 9; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTLK 4
| |
Db 1 LPLR 4

RESULT 12
CHOX_ALCSP STANDARD; PRT; 7 AA.
ID CHOX_ALCSP STANDARD; PRT; 7 AA.
AC P16101;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Choline oxidase (EC 1.1.3.17) (Fragment).
OS Alcaligenes sp.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Alcaligenes.
OX NCBI_TaxID=512;
RN [1]
RP SEQUENCE.
RX MEDLINE=81006769; PubMed=6997283;
RA Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.;
RT "Identification and properties of the prosthetic group of choline
oxidase from *Alcaligenes* sp.";
RL J. Biochem. 88:197-203(1980).
CC -!- CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2).
DR PIR; A15398; A15398.
KW Direct protein sequencing; Oxidoreductase.
FT NON_TER 7
SQ SEQUENCE 7 AA; 839 MW; 7415B1E457644AC0 CRC64;

Query Match 29.0%; Score 9; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SR 7
| |
Db 6 SR 7

RESULT 13
UC24_MAIZE STANDARD; PRT; 7 AA.
ID UC24_MAIZE STANDARD; PRT; 7 AA.
AC P80630;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 447) (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi P., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
genome analysis program";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
protein is: 6.0, its MW is: 30.0 kDa.
DR Maize-2DPAGE; P80630; COLEOPTILE.
DR MaizeDB; 123956; -.
KW Direct protein sequencing.
FT NON_TER 1 1

Query Match 32.3%; Score 10; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTL 3
: | |
Db 1 VTL 3

RESULT 10
Q08433 PRELIMINARY; PRT; 4 AA.
AC Q08433;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Bilirubin UDP-glucuronosyltransferase (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gunn;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koiwai O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
DR EMBL; S38636; AAB19259.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Transferase.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 29.0%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LX 4
| |
Db 3 LX 4

RESULT 11
FARP_CHICK STANDARD; PRT; 5 AA.
ID FARP_CHICK STANDARD; PRT; 5 AA.
AC P83308;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRamide-like neuropeptide (LPLRF-amide).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RX PubMed=6137771;
RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
RT "A novel active pentapeptide from chicken brain identified by
antibodies to FMRamide";
RL Nature 305:328-330(1983).
CC -!- FUNCTION: May function as a neurotransmitter or modulator.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 5 5 Phenylalanine amide.

FT NON TER 7 7
SQ SEQUENCE 7 AA; 665 MW; 6DC1B5B33DC1B5D0 CRC64;
Query Match 29.0%; Score 9; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 TLK 4
Db 2 TAK 4

RESULT 14
Q15897
ID Q15897 PRELIMINARY; PRT; 7 AA.
AC Q15897;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Homo sapiens (clone XP6A11A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries."
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32077; AAA73887.1; -.
FT NON TER 1 1
FT NON TER 7 7
SQ SEQUENCE 7 AA; 814 MW; 672B1DD3372046B0 CRC64;

Query Match 29.0%; Score 9; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LK 4
Db 3 LK 4

RESULT 15
P93233
ID P93233 PRELIMINARY; PRT; 7 AA.
AC P93233;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
DE (Fragment).
GN Name=LE-ACS1B;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97351561; PubMed=9207843;
RA Oetiker J.H.; Olson D.C.; Shiu O.Y., Yang S.F.;
RT "Differential induction of seven 1-aminocyclopropane-1-carboxylate
RT synthase genes by elicitor in suspension cultures of tomato
RT (Lycopersicon esculentum).";
RL Plant Mol. Biol. 34:275-286(1997).
DR EMBL; U75692; AAC49682.1; -.
DR GO; GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.

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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:54:10 ; Search time 92.3333 Seconds
(without alignments)
27.196 Million cell updates/sec

Title: US-09-712-819D-13
Perfect score: 31
Sequence: 1 LTLKLSR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 116873

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: _geneseqp1980s:*
2: _geneseqp1990s:*
3: _geneseqp2000s:*
4: _geneseqp2001s:*
5: _geneseqp2002s:*
6: _geneseqp2003as:*
7: _geneseqp2003bs:*
8: _geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	20	64.5	7	5	ABP66518 Human RSV
2	20	64.5	7	6	ABU69381 Respirato
3	20	64.5	7	7	AGE35876 SYNAGIS a
4	20	64.5	7	8	ADI57038 RSV antib
5	19	61.3	7	2	AAW69269 Haemagglu
6	19	61.3	7	2	AAY42013 Rheumatoi
7	19	61.3	7	2	AAY41889 Rheumatoi
8	19	61.3	7	4	ABB55870 Vascular
9	19	61.3	7	4	ABB56283 Vascular
10	19	61.3	7	4	ABB55981 Vascular
11	19	61.3	7	4	AAU28602 DPI trypt
12	19	61.3	7	4	AAU24969 Schizoph
13	19	61.3	7	4	AAU26249 Depressio
14	19	61.3	7	4	AAU15313 Schizoph
15	19	61.3	7	4	ABB52355 Human API
16	19	61.3	7	5	ABP66489 Human RSV
17	19	61.3	7	5	ABG78901 Multiple
18	19	61.3	7	5	ABG78730 Multiple
19	19	61.3	7	6	ABP58010 Prostate
20	19	61.3	7	6	ABU69352 Respirato
21	19	61.3	7	6	ABP57255 Breast ca
22	19	61.3	7	6	ABR59042 Alzheimer
23	19	61.3	7	7	ADE35847 SYNAGIS a
24	19	61.3	7	8	ADH35821 Vitamin D
25	19	61.3	7	8	ADH35827 Vitamin D

26	19	61.3	7	8	ADI57009 RSV antib
27	19	61.3	7	8	ADN32134 Human Alz
28	19	61.3	7	8	ADO78580 Schizophr
29	18	58.1	6	5	Aae21359 S. cerevi
30	18	58.1	7	2	AAW82668 Cauliflow
31	18	58.1	7	3	AAB02931 Nucleotid
32	18	58.1	7	4	AAE10492 Humanised
33	18	58.1	7	5	ABP66389 Human RSV
34	18	58.1	7	5	ABP66450 Human RSV
35	18	58.1	7	5	ABP66485 Human RSV
36	18	58.1	7	5	ABP49796 Zinc fing
37	18	58.1	7	5	ABP48455 Zinc fing
38	18	58.1	7	5	ABP51172 Zinc fing
39	18	58.1	7	5	ABP49577 Zinc fing
40	18	58.1	7	5	ABP49790 Zinc fing
41	18	58.1	7	5	ABB07139 Human ery
42	18	58.1	7	5	AAE28044 Human mod
43	18	58.1	7	6	ABU69348 Respirato
44	18	58.1	7	6	ABU69252 Respirato
45	18	58.1	7	6	ABU69313 Respirato

ALIGNMENTS

RESULT 1
ABP66518
ID ABP66518 standard; peptide; 7 AA.
XX
AC ABP66518;
XX
DT 04-DEC-2002 (first entry)
XX
DE Human RSV antibody VL CDR2 fragment.
XX
KW Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;
KW complementarity determining region; respiratory syncytial virus;
KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;
KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;
KW bronchopulmonary dysplasia; congenital heart disease;
KW congenital immunodeficiency; acquired immunodeficiency.
OS Homo sapiens.
XX
PN WO200243660-A2.
XX
PD 06-JUN-2002.
XX
PF 28-NOV-2001; 2001WO-US044807.
XX
PR 28-NOV-2000; 2000US-00724396.
PR 28-NOV-2000; 2000US-00724531.
XX
PA (MEDI-) MEDIUMMUNE INC.
XX
PI Young JF, Koenig S, Johnson LS;
XX WPI; 2002-706803/76.
DR
XX Antibody for treating respiratory syncytial virus (RSV) infection,
PT comprises a variable heavy/light domain or complementarity determining
PT regions 1 - 3 of variable light/heavy chains, that immunospecifically
PT binds to RSV antigen.
XX
PS Claim 8; Page 55; 298pp; English.
XX
CC The invention relates to a novel antibody comprising a variable heavy
CC (VH) domain, variable light (VL) domain, VH complementarity determining
CC region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the
CC antibody immunospecifically binds to a respiratory syncytial virus (RSV)
CC antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,
CC and immunostimulant activity. The polynucleotides of the invention may

CC have a use in a vaccine, and in gene therapy. The antibody is useful for
CC treating or ameliorating a RSV infection in a human. The antibody is also
CC useful for preventing, treating or ameliorating one or more symptoms
CC associated with RSV infection in a mammal, e.g. cystic fibrosis,
CC bronchopulmonary dysplasia, congenital heart disease, congenital
CC immunodeficiency or acquired immunodeficiency, or after a bone marrow
CC transplant. The sequence represents a complementary determining region
CC peptide from a human RSV antibody of the invention
XX
SQ Sequence 7 AA;

Query Match 64.5%; Score 20; DB 5; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLS 6
Db 2 TMKLS 6

RESULT 2
ABU69381

ID ABU69381 standard; peptide; 7 AA.
XX
AC ABU69381;
XX
DT 03-JUN-2003 (first entry)
XX
DE Respiratory syncytial virus (RSV) antibody fragment #126.
XX
KW Respiratory syncytial virus; RSV; vaccine; antibody;
KW variable heavy domain; VH; variable light domain; VL;
KW complementarity determining region; CDR; CDR1; CDR2; CDR3; RSV infection;
KW cystic fibrosis; bronchopulmonary dysplasia; congenital heart disease;
KW congenital immunodeficiency; acquired immune deficiency;
KW bone marrow transplant.
XX
OS Homo sapiens.
XX
PN US2002177126-A1.
XX
PD 28-NOV-2002.
XX
PF 28-NOV-2001; 2001US-00996288.
XX
PR 28-NOV-2000; 2000US-00724531.
XX
PA (MEDI-) MEDIMMUNE INC.
XX
PI Young JF, Koenig S, Johnson LS;
XX
DR WPI; 2003-340947/32.
XX
PT New antibody comprising a variable heavy (VH) or variable light (VL)
PT domain or complementarity determining region (CDR), such as CDR1, CDR2,
PT or CDR3, useful for preventing or treating a respiratory syncytial virus
PT (RSV) infection.
XX
PS Claim 8; Page 24; 165pp; English.
XX
CC The invention describes an antibody comprising a variable heavy (VH) or
CC variable light (VL) domain or complementarity determining region (CDR),
CC such as CDR1, CDR2, or CDR3, which immunospecifically binds to a
CC respiratory syncytial virus (RSV) antigen and is not SYNAGIS (RTM). The
CC antibody, pharmaceutical compositions and methods are useful for
CC preventing, treating or ameliorating a RSV infection in patients with
CC cystic fibrosis, bronchopulmonary dysplasia, congenital heart disease,
CC congenital immunodeficiency, or acquired immune deficiency, or patients
CC having had a bone marrow transplant or the elderly. This is the amino
CC acid sequence of a respiratory syncytial virus (RSV) antibody peptide
XX
SQ Sequence 7 AA;

Query Match 64.5%; Score 20; DB 6; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLS 6
Db 2 TMKLS 6

RESULT 3
ADE35876

ID ADE35876 standard; peptide; 7 AA.
XX
AC ADE35876;
XX
DT 29-JAN-2004 (first entry)
XX
DE SYNAGIS antibody based light chain variable region 2, VL2, CDR #54.
XX
KW respiratory syncytial virus; RSV infection; high affinity antibody;
KW high avidity antibody; low antibody dose; more effective prophylaxis;
KW complementarity determining region; CDR; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US2003091584-A1.
XX
PD 15-MAY-2003.
XX
PF 28-NOV-2001; 2001US-00996265.
XX
PR 28-NOV-2000; 2000US-00724396.
XX
PA (YOUNG) YOUNG J F.
PA (KOENIG) KOENIG S.
PA (JOHN) JOHNSON L S.
XX
PI Young JF, Koenig S, Johnson LS;
XX
DR WPI; 2003-874589/81.
XX
PT Preventing, treating or ameliorating symptoms associated with respiratory
PT syncytial virus infection in mammal by administering antibodies or their
PT fragments that immunospecifically bind to RSV antigens.
XX
PS Claim 111; SEQ ID NO 164; 161pp; English.
XX
CC The invention relates to a method of preventing, treating or ameliorating
CC one or more symptoms associated with a respiratory syncytial virus (RSV)
CC infection in a mammal. A sustained release formulation comprising one or
CC more antibodies or their fragments that immunospecifically bind to one or
CC more RSV antigens and a pharmaceutical composition comprising one or more
CC antibodies or their fragments that immunospecifically bind to one or more
CC RSV antigens formulated for pulmonary delivery is useful for preventing,
CC treating or ameliorating one or more symptoms associated with a RSV
CC infection in a mammal by administering the formulation to the mammal, or
CC the composition to the lungs of the mammal. The antibodies bind to RSV
CC antigen with a high affinity and/or high avidity. The methods use lower
CC doses of antibodies which immunospecifically bind to RSV antigen, and
CC which provide a more effective prophylaxis. The present sequence
CC represents the amino acid sequence of a complementarity determining
CC region based on the SYNAGIS antibody.
XX
SQ Sequence 7 AA;

Query Match 64.5%; Score 20; DB 7; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLS 6
Db 2 TMKLS 6

Thu Nov 4 07:26:52 2004

XX
PN WO9947925-A2.
XX
PD 23-SEP-1999.
XX
PF 15-MAR-1999; 99WO-GB0000763.
XX
PR 13-MAR-1998; 98GB-00005477.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Parekh RB, Patel TP, Townsend RR;
XX
DR WPI; 1999-571871/48.
XX
PT Diagnosis of human rheumatoid arthritis by two-dimensional electrophoresis.
XX
PS Disclosure; Page 21; 157pp; English.
XX
CC A method has been developed for the diagnosis of human rheumatoid arthritis (RA) using two-dimensional electrophoresis to generate a two-dimensional array of features. The method can be used for screening, diagnosis and prognosis of RA in a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method comprises: (a) analysing a sample of serum or plasma and optionally synovial fluid by two-dimensional electrophoresis, to generate a two-dimensional array of features; (b) identifying at least one chosen feature whose relative abundance correlates with the presence or absence of RA; and (c) comparing the abundance of each chosen feature in the sample with the abundance of that chosen feature in serum or plasma from one or more persons without RA, where the relative abundance of the chosen feature or features in the sample indicates the presence or absence of RA in the subject. The method can also be used in clinical studies for testing drugs for therapy of RA, for purification of RA-diagnostic protein isoforms (RPIs), and for production of antibodies to RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify compounds that promote or inhibit their activity, which are then used as RA drugs. Nucleic acid encoding RADFs can be used in gene therapy protocols. AAY41844 to AAY42100 represent RPI peptides, AAY42101 to AAY42103 represent expression reference protein isoform peptides and AAZ25066 to AAZ25068 represent degenerate probes for RPIs, which are all used in the exemplification of the present invention
XX
SQ Sequence 7 AA;
Query Match 61.3%; Score 19; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 TLKLSR 7
Db 2 TLMISR 7
RESULT 7
AAY41889
ID AAY41889 standard; peptide; 7 AA.
XX
AC AAY41889;
XX
DT 09-DEC-1999 (first entry)
XX
DE Rheumatoid arthritis diagnostic protein isoform peptide #40.
KW Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;
KW rheumatoid arthritis diagnostic feature; ERPI; synovial fluid;
KW rheumatoid arthritis diagnostic protein isoform; screening;
XX expression reference protein isoform; prognosis.
OS Homo sapiens.
XX
PN WO9947925-A2.

XX
PD 23-SEP-1999.
XX
PF 15-MAR-1999; 99WO-GB0000763.
XX
PR 13-MAR-1998; 98GB-00005477.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Parekh RB, Patel TP, Townsend RR;
XX
DR WPI; 1999-571871/48.
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PT Diagnosis of human rheumatoid arthritis by two-dimensional electrophoresis.
XX
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XX
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XX
SQ Sequence 7 AA;
Query Match 61.3%; Score 19; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 TLKLSR 7
Db 2 TLMISR 7
RESULT 7
AAY41889
ID AAY41889 standard; peptide; 7 AA.
XX
AC AAY41889;
XX
DT 09-DEC-1999 (first entry)
XX
DE Rheumatoid arthritis diagnostic protein isoform peptide #40.
KW Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;
KW rheumatoid arthritis diagnostic feature; ERPI; synovial fluid;
KW rheumatoid arthritis diagnostic protein isoform; screening;
XX expression reference protein isoform; prognosis.
OS Homo sapiens.
XX
PN WO9947925-A2.

XX
PD 23-SEP-1999.
XX
PF 15-MAR-1999; 99WO-GB0000763.
XX
PR 13-MAR-1998; 98GB-00005477.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Parekh RB, Patel TP, Townsend RR;
XX
DR WPI; 1999-571871/48.
XX
PT Diagnosis of human rheumatoid arthritis by two-dimensional electrophoresis.
XX
PS Disclosure; Page 18; 157pp; English.
XX
CC A method has been developed for the diagnosis of human rheumatoid arthritis (RA) using two-dimensional electrophoresis to generate a two-dimensional array of features. The method can be used for screening, diagnosis and prognosis of RA in a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method comprises: (a) analysing a sample of serum or plasma and optionally synovial fluid by two-dimensional electrophoresis, to generate a two-dimensional array of features; (b) identifying at least one chosen feature whose relative abundance correlates with the presence or absence of RA; and (c) comparing the abundance of each chosen feature in the sample with the abundance of that chosen feature in serum or plasma from one or more persons without RA, where the relative abundance of the chosen feature or features in the sample indicates the presence or absence of RA in the subject. The method can also be used in clinical studies for testing drugs for therapy of RA, for purification of RA-diagnostic protein isoforms (RPIs), and for production of antibodies to RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify compounds that promote or inhibit their activity, which are then used as RA drugs. Nucleic acid encoding RADFs can be used in gene therapy protocols. AAY41844 to AAY42100 represent RPI peptides, AAY42101 to AAY42103 represent expression reference protein isoform peptides and AAZ25066 to AAZ25068 represent degenerate probes for RPIs, which are all used in the exemplification of the present invention
XX
SQ Sequence 7 AA;
Query Match 61.3%; Score 19; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 TLKLSR 7
Db 2 TFLSLR 7
RESULT 8
ABB55870
ID ABB55870 standard; peptide; 7 AA.
XX
AC ABB55870;
XX
DT 15-FEB-2002 (first entry)
XX
DE Vascular dementia-associated protein isoform (VPI) 70.
KW Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
KW diagnosis; prognosis; gene therapy.
XX Homo sapiens.
OS
PN WO200169261-A2.
XX
PD 20-SEP-2001.
XX
PF 14-MAR-2001; 2001WO-GB001106.

XX
PD 23-SEP-1999.
XX
PF 15-MAR-1999; 99WO-GB0000763.
XX
PR 13-MAR-1998; 98GB-00005477.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Parekh RB, Patel TP, Townsend RR;
XX
DR WPI; 1999-571871/48.
XX
PT Diagnosis of human rheumatoid arthritis by two-dimensional electrophoresis.
XX
PS Disclosure; Page 18; 157pp; English.
XX
CC A method has been developed for the diagnosis of human rheumatoid arthritis (RA) using two-dimensional electrophoresis to generate a two-dimensional array of features. The method can be used for screening, diagnosis and prognosis of RA in a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method comprises: (a) analysing a sample of serum or plasma and optionally synovial fluid by two-dimensional electrophoresis, to generate a two-dimensional array of features; (b) identifying at least one chosen feature whose relative abundance correlates with the presence or absence of RA; and (c) comparing the abundance of each chosen feature in the sample with the abundance of that chosen feature in serum or plasma from one or more persons without RA, where the relative abundance of the chosen feature or features in the sample indicates the presence or absence of RA in the subject. The method can also be used in clinical studies for testing drugs for therapy of RA, for purification of RA-diagnostic protein isoforms (RPIs), and for production of antibodies to RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify compounds that promote or inhibit their activity, which are then used as RA drugs. Nucleic acid encoding RADFs can be used in gene therapy protocols. AAY41844 to AAY42100 represent RPI peptides, AAY42101 to AAY42103 represent expression reference protein isoform peptides and AAZ25066 to AAZ25068 represent degenerate probes for RPIs, which are all used in the exemplification of the present invention
XX
SQ Sequence 7 AA;
Query Match 61.3%; Score 19; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 TLKLSR 7
Db 2 TFLSLR 7
RESULT 8
ABB55870
ID ABB55870 standard; peptide; 7 AA.
XX
AC ABB55870;
XX
DT 15-FEB-2002 (first entry)
XX
DE Vascular dementia-associated protein isoform (VPI) 70.
KW Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
KW diagnosis; prognosis; gene therapy.
XX Homo sapiens.
OS
PN WO200169261-A2.
XX
PD 20-SEP-2001.
XX
PF 14-MAR-2001; 2001WO-GB001106.

XX 15-MAR-2000; 2000GB-00006285.
 PR 24-NOV-2000; 2000GB-00028734.
 PR 28-NOV-2000; 2000US-00724391.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PA Herath HMac, Parekh RB, Rohlf C;
 XX WPI; 2001-557937/62.
 PI Screening, diagnosis or prognosis of vascular dementia (VD), useful for
 XX determining stage of VD and monitoring the effect of VD therapy,
 PT comprises analyzing body fluid by 2-dimensional electrophoresis for
 PT features correlated with VD.
 XX Claim 6; Page 31; 151pp; English.
 PS The invention relates to screening, diagnosis or prognosis of Vascular
 XX Dementia (VD) in a subject comprising analysing body fluid from the
 CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
 CC features containing at least one chosen feature whose relative abundance
 CC correlates with the presence, absence, stage or severity of VD or
 CC predicts the onset or course of VD, especially detecting in a sample of
 CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
 CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
 CC specification. Detecting VD-associated features and VPI is useful for the
 CC screening, diagnosis or prognosis of VD, for determining the stage or
 CC severity of VD, for identifying a subject at risk of VD or for monitoring
 CC the effect of therapy administered to a subject having VD. Nucleic acids
 CC encoding a VPI or inhibiting the function of a VPI are useful for the
 CC treatment of VD and for gene therapy
 XX Sequence 7 AA;
 SQ Query Match 61.3%; Score 19; DB 4; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 TLKLSR 7
 Db | : |||
 2 TFEISR 7
 RESULT 9
 ABB56283
 ID ABB56283 standard; peptide; 7 AA.
 XX ABB56283;
 AC
 DT 15-FEB-2002 (first entry)
 XX Vascular dementia-associated protein isoform (VPI) 483.
 DE Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
 KW diagnosis; prognosis; gene therapy.
 KW Homo sapiens.
 OS WO200169261-A2.
 XX 20-SEP-2001.
 PD 14-MAR-2001; 2001WO-GB001106.
 XX 15-MAR-2000; 2000GB-00006285.
 PR 24-NOV-2000; 2000GB-00028734.
 PR 28-NOV-2000; 2000US-00724391.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PA Herath HMac, Parekh RB, Rohlf C;
 XX WPI; 2001-557937/62.

DR WPI; 2001-557937/62.
 XX Screening, diagnosis or prognosis of vascular dementia (VD), useful for
 PT determining stage of VD and monitoring the effect of VD therapy,
 PT comprises analyzing body fluid by 2-dimensional electrophoresis for
 PT features correlated with VD.
 XX Claim 6; Page 40; 151pp; English.
 PS The invention relates to screening, diagnosis or prognosis of Vascular
 XX Dementia (VD) in a subject comprising analysing body fluid from the
 CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
 CC features containing at least one chosen feature whose relative abundance
 CC correlates with the presence, absence, stage or severity of VD or
 CC predicts the onset or course of VD, especially detecting in a sample of
 CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
 CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
 CC specification. Detecting VD-associated features and VPI is useful for the
 CC screening, diagnosis or prognosis of VD, for determining the stage or
 CC severity of VD, for identifying a subject at risk of VD or for monitoring
 CC the effect of therapy administered to a subject having VD. Nucleic acids
 CC encoding a VPI or inhibiting the function of a VPI are useful for the
 CC treatment of VD and for gene therapy
 XX Sequence 7 AA;
 SQ Query Match 61.3%; Score 19; DB 4; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 TLKLSR 7
 Db | : |||
 2 TFEISR 7
 RESULT 10
 ABB55981
 ID ABB55981 standard; peptide; 7 AA.
 XX ABB55981;
 AC
 DT 15-FEB-2002 (first entry)
 XX Vascular dementia-associated protein isoform (VPI) 181.
 DE Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
 KW diagnosis; prognosis; gene therapy.
 KW Homo sapiens.
 OS WO200169261-A2.
 XX 20-SEP-2001.
 PD 14-MAR-2001; 2001WO-GB001106.
 XX 15-MAR-2000; 2000GB-00006285.
 PR 24-NOV-2000; 2000GB-00028734.
 PR 28-NOV-2000; 2000US-00724391.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PA Herath HMac, Parekh RB, Rohlf C;
 XX WPI; 2001-557937/62.
 PI Screening, diagnosis or prognosis of vascular dementia (VD), useful for
 XX determining stage of VD and monitoring the effect of VD therapy,
 PT comprises analyzing body fluid by 2-dimensional electrophoresis for
 PT features correlated with VD.
 XX Claim 6; Page 33; 151pp; English.
 PS
 XX

CC The invention relates to screening, diagnosis or prognosis of Vascular
CC Dementia (VD) in a subject comprising analysing body fluid from the
CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
CC features containing at least one chosen feature whose relative abundance
CC correlates with the presence, absence, stage or severity of VD or
CC predicts the onset or course of VD, especially detecting in a sample of
CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
CC specification. Detecting VD-associated features and VPI is useful for the
CC screening, diagnosis or prognosis of VD, for determining the stage or
CC severity of VD, for identifying a subject at risk of VD or for monitoring
CC the effect of therapy administered to a subject having VD. Nucleic acids
CC encoding a VPI or inhibiting the function of a VPI are useful for the
CC treatment of VD and for gene therapy
XX
SQ Sequence 7 AA;

Query Match 61.3%; Score 19; DB 4; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLKLSR 7
Db 2 TFELSR 7

RESULT 11
AAU28602
ID AAU28602 standard; peptide; 7 AA.
XX
AC AAU28602;
XX
DT 03-JAN-2002 (first entry)
XX
DE DPI tryptic digest peptide #199.
XX
KW Human; depression associated protein isoform; tryptic digest peptide;
KW DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
KW maniac-depressive illness; schizoaffective disorder.
XX
OS Homo sapiens.
XX
PN WO200162787-A1.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-GB000786.
XX
PR 24-FEB-2000; 2000GB-00004412.
PR 08-DEC-2000; 2000GB-00030050.
PR 12-DEC-2000; 2000US-0254830P.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;
XX
DR WPI; 2001-570626/64.
XX
PT Novel nucleic acid encoding a protein associated with bipolar affective
PT disorder, which is used for diagnosis, prophylaxis and therapy of
PT neuropsychiatric disorders, such as bipolar affective disorder.
XX
PS Disclosure; Page 34; 153pp; English.
XX
CC The present invention relates to the identification of depression
CC associated protein isoforms (DPIs), particularly the tryptic digest
CC peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)
CC described are decreased in the cerebrospinal fluid (CSF) of BAD (bipolar
CC affective disorder) subjects, whilst other DPIs (AAU28626-AAU28887) are
CC increased in BAD subjects. Also described are peptide sequences
CC identified from DPI-45 and DPI-213 and the nucleic acid sequence they are
CC encoded by. The sequences of the invention are useful for clinical

CC screening, diagnosis, prognosis, therapy and prophylaxis of
CC neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder,
CC BP), maniac-depressive illnesses, attention deficit disorders,
CC schizoaffective disorders, and unipolar affective disorders. The present
CC sequence represents one of the DPI tryptic digest peptides of the present
CC invention
XX
SQ Sequence 7 AA;

Query Match 61.3%; Score 19; DB 4; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLKLSR 7
Db 2 TFELSR 7

RESULT 12
AAU24969
ID AAU24969 standard; peptide; 7 AA.
XX
AC AAU24969;
XX
DT 18-DEC-2001 (first entry)
XX
DE Schizophrenia-Associated Protein Isoform (SPI) peptide #198.
XX
KW Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;
KW neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
XX
OS Homo sapiens.
XX
PN WO200162785-A2.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-GB000792.
XX
PR 24-FEB-2000; 2000GB-00004415.
PR 28-DEC-2000; 2000US-00750395.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;
XX
DR WPI; 2001-570624/64.
XX
PT New schizophrenia associated protein isoforms and encoding nucleic acid
PT molecules, useful for treatment, diagnosis and prognosis of schizophrenia
PT and screening for potential drugs for treatment and new drug targets.
XX
PS Disclosure; Page 32; 148pp; English.
XX
CC The sequence represents a schizophrenia-associated protein isoform (SPI).
CC These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable
CC in cerebrospinal fluid, serum or plasma and are useful markers of
CC schizophrenia. The sequences can be used for treatment and diagnosis of
CC schizophrenia, screening, prognosis, monitoring the results of therapy,
CC identifying patients most likely to respond to a particular therapy and
CC identification of new targets for drug treatment. SPI DNA is useful as a
CC nucleic acid probe to detect the presence of nucleic acids or SPIs
XX
SQ Sequence 7 AA;

Query Match 61.3%; Score 19; DB 4; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLKLSR 7
Db 2 TFELSR 7

XX 08-FEB-2002 (first entry)
DT Human API-125 tryptic digest peptide #8.
XX
DE
XX
KW Human; neuroprotective; nootropic; gene therapy; vaccine;
KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
KW Expression Reference Protein Isoform; ERPI; proteolysis.
XX
OS Homo sapiens.
XX
PN WO200175454-A2.
XX
PD 11-OCT-2001.
XX
PF 03-APR-2001; 2001WO-US010908.
XX
PR 03-APR-2000; 2000US-0194504P.
PR 28-NOV-2000; 2000US-0253647P.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA (PFIZ) PFIZER INC.
XX
PI Durham KL, Friedman DL, Herath HMAC, Kimmel LH, Parekh RB;
PI Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;
PI Townsend RR, White F, Williams SA;
XX
DR WPI; 2001-639384/73.
XX
PT Screening for Alzheimer's disease in a mammal, by making two-dimensional
PT array of a feature whose relative abundance correlates with disease, and
PT comparing with abundance of the feature in samples of healthy persons.
XX
PS Example; Page 34; 162pp; English.
XX
CC The invention relates to methods for the screening, diagnosis and
CC prognosis of Alzheimer's disease. The methods involve the detection of
CC Alzheimer's Disease-Associated Features (AFs) and Alzheimer's Disease-
CC Associated Protein Isoforms (APIs) in cerebrospinal fluid, serum or
CC plasma. The abundance of the AFs and APIs is then normalised to an
CC Expression Reference Protein Isoform (ERPI) in order to determine whether
CC a patient is suffering from, or has a predisposition to, Alzheimer's
CC Disease. The relative abundance of the AFs and APIs correlates with the
CC severity of Alzheimer's Disease. The present sequence is a peptide
CC produced from an API by proteolysis
XX
SQ Sequence 7 AA;
Query Match 61.3%; Score 19; DB 4; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLKLSR 7
| : |||
Db 2 TFEISR 7

Search completed: November 4, 2004, 01:18:16
Job time : 94.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 01:23:27 ; Search time 69.3333 Seconds
(without alignments)
32.733 Million cell updates/sec

Title: US-09-712-819D-13
Perfect score: 31
Sequence: 1 LTKLSR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 56143

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	20	64.5	7	9	US-09-996-288-164
2	20	64.5	7	10	US-09-996-265-164
3	20	64.5	7	15	US-10-461-863-164
4	19	61.3	7	9	US-09-791-378-198
5	19	61.3	7	9	US-09-998-909-7
6	19	61.3	7	9	US-09-826-290-370
7	19	61.3	7	9	US-09-996-288-135
8	19	61.3	7	10	US-09-791-393-145
9	19	61.3	7	10	US-09-791-389-145
10	19	61.3	7	10	US-09-996-265-135
11	19	61.3	7	11	US-09-791-377-198
12	19	61.3	7	13	US-10-044-034-13
13	19	61.3	7	15	US-10-461-863-135

14	19	61.3	7	15	US-10-264-309-460	Sequence 460, App
15	19	61.3	7	15	US-10-601-100-105	Sequence 105, App
16	19	61.3	7	17	US-10-700-340-154	Sequence 154, App
17	18	58.1	6	9	US-09-897-107-24	Sequence 24, Appl
18	18	58.1	7	9	US-09-989-789-396	Sequence 396, App
19	18	58.1	7	9	US-09-989-789-1971	Sequence 1971, Ap
20	18	58.1	7	9	US-09-989-789-3503	Sequence 3503, Ap
21	18	58.1	7	9	US-09-989-789-3542	Sequence 3542, Ap
22	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, Ap
23	18	58.1	7	9	US-09-796-848A-20	Sequence 20, Appl
24	18	58.1	7	9	US-09-844-508-43	Sequence 43, Appl
25	18	58.1	7	9	US-09-996-288-35	Sequence 35, Appl
26	18	58.1	7	9	US-09-996-288-96	Sequence 96, Appl
27	18	58.1	7	9	US-09-996-288-131	Sequence 131, App
28	18	58.1	7	10	US-09-990-186-396	Sequence 396, App
29	18	58.1	7	10	US-09-990-186-1971	Sequence 1971, Ap
30	18	58.1	7	10	US-09-990-186-3503	Sequence 3503, Ap
31	18	58.1	7	10	US-09-990-186-3542	Sequence 3542, Ap
32	18	58.1	7	10	US-09-990-186-3544	Sequence 3544, Ap
33	18	58.1	7	10	US-09-996-265-35	Sequence 35, Appl
34	18	58.1	7	10	US-09-996-265-96	Sequence 96, Appl
35	18	58.1	7	10	US-09-996-265-131	Sequence 131, App
36	18	58.1	7	10	US-09-989-994-396	Sequence 396, App
37	18	58.1	7	10	US-09-989-994-1971	Sequence 1971, Ap
38	18	58.1	7	10	US-09-989-994-3503	Sequence 3503, Ap
39	18	58.1	7	10	US-09-989-994-3542	Sequence 3542, Ap
40	18	58.1	7	10	US-09-989-994-3544	Sequence 3544, Ap
41	18	58.1	7	14	US-10-084-826-43	Sequence 43, Appl
42	18	58.1	7	14	US-10-234-026-6	Sequence 6, Appli
43	18	58.1	7	14	US-10-020-354-35	Sequence 35, Appl
44	18	58.1	7	15	US-10-461-863-35	Sequence 35, Appl
45	18	58.1	7	15	US-10-461-863-96	Sequence 96, Appl

ALIGNMENTS

RESULT 1
US-09-996-288-164
; Sequence 164, Application US/09996288
; Patent No. US2002017126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylax
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 164
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-164

Query Match 64.5%; Score 20; DB 9; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLS 6
|:|:|
Db 2 TMKLS 6

RESULT 2
US-09-996-265-164
; Sequence 164, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James


```
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 164
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-996-265-164

Query Match      64.5%; Score 20; DB 10; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 TLKLS 6
      |:|
Db      2 TMKLS 6

RESULT 3
US-10-461-863-164
; Sequence 164, Application US/10461863
; Publication No. US20040018200A1
; GENERAL INFORMATION:
; APPLICANT: Oliver, Cynthia
; APPLICANT: Allan, Christian
; APPLICANT: Chang, Stephen
; TITLE OF INVENTION: STABILIZED ANTI-RESPIRATORY SYNCYTIAL VIRUS (RSV) ANTIBODY FORMUL
; FILE REFERENCE: 10271-071-999
; CURRENT APPLICATION NUMBER: US/10/461,863
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: 60/388,920
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 209
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 164
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-461-863-164

Query Match      64.5%; Score 20; DB 15; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 TLKLS 6
      |:|
Db      2 TMKLS 6

RESULT 4
US-09-791-378-198
; Sequence 198, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791,378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 198
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-791-378-198
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; ORGANISM: Homo sapiens
US-09-791-378-198

Query Match      61.3%; Score 19; DB 9; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 TLKLSR 7
      |:|
Db      2 TFELSR 7

RESULT 5
US-09-998-909-7
; Sequence 7, Application US/09998909
; Patent No. US20020164664A1
; GENERAL INFORMATION:
; APPLICANT: Hlavaty, John
; APPLICANT: Briggman, Joseph
; TITLE OF INVENTION: Detection and Treatment of Prostate Cancer
; FILE REFERENCE: MTP-027
; CURRENT APPLICATION NUMBER: US/09/998,909
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/250,284
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-998-909-7

Query Match      61.3%; Score 19; DB 9; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 TLKLSR 7
      |:|
Db      2 TFELSR 7

RESULT 6
US-09-826-290-370
; Sequence 370, Application US/09826290
; Patent No. US20020164668A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L. Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlf, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 370
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; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-370

Query Match
Best Local Similarity 61.3%; Score 19; DB 9; Length 7;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLKLSR 7
Db 2 TFELSR 7

RESULT 7
US-09-996-288-135
; Sequence 135, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 135
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-135

Query Match
Best Local Similarity 61.3%; Score 19; DB 9; Length 7;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLS 6
Db 2 TLKLA 6

RESULT 8
US-09-791-393-145
; Sequence 145, Application US/09791393
; Publication No. US20030032200A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-393-145

Query Match
61.3%; Score 19; DB 10; Length 7;
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Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLKLSR 7
Db 2 TFELSR 7

RESULT 9
US-09-791-389-145
; Sequence 145, Application US/09791389
; Publication No. US20030032773A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; APPLICANT: Terrett, Jonathan Alexander
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; FILE REFERENCE: 2543-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/791,389
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GB 0004412.3
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GB 0030050.9
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/254,830
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-389-145
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Query Match
Best Local Similarity 61.3%; Score 19; DB 10; Length 7;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLKLSR 7
Db 2 TFELSR 7

RESULT 10
US-09-996-265-135
; Sequence 135, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 135
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-135

Query Match
Best Local Similarity 61.3%; Score 19; DB 10; Length 7;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLS 6
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Db 2 TLKLA 6

RESULT 11
US-09-791-377-198
; Sequence 198, Application US/09791377
; Publication No. US20040110938A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-060-999
; CURRENT APPLICATION NUMBER: US/09/791,377
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 198
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-377-198

Query Match 61.3%; Score 19; DB 11; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLKLSR 7
Db 2 TFEISR 7

RESULT 12
US-10-044-034-13
; Sequence 13, Application US/10044034
; Publication No. US20020169264A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, DAVID C.
; APPLICANT: O'BRIEN-SIMPSON, NEIL M.
; APPLICANT: BROWN, LORENA E.
; APPLICANT: EDE, NICHOLAS J.
; APPLICANT: BRANDT, EVELYN R.
; APPLICANT: GOOD, MICHAEL F.
; TITLE OF INVENTION: POLYMERS INCORPORATING PEPTIDES
; FILE REFERENCE: FBRC:006
; CURRENT APPLICATION NUMBER: US/10/044,034
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: P05071
; PRIOR FILING DATE: 1997-02-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptides
US-10-044-034-13

Query Match 61.3%; Score 19; DB 13; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLS 6
Db 1 TLKLA 5

RESULT 13
US-10-461-863-135

; Sequence 135, Application US/10461863
; Publication No. US20040018200A1
; GENERAL INFORMATION:
; APPLICANT: Oliver, Cynthia
; APPLICANT: Allan, Christian
; APPLICANT: Chang, Stephen
; TITLE OF INVENTION: STABILIZED ANTI-RESPIRATORY SYNCYTIAL VIRUS (RSV) ANTIBODY FORMUL
; FILE REFERENCE: 10271-071-999
; CURRENT APPLICATION NUMBER: US/10/461,863
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: 60/388,920
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 209
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 135
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-461-863-135

Query Match 61.3%; Score 19; DB 15; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLS 6
Db 2 TLKLA 6

RESULT 14
US-10-264-309-460
; Sequence 460, Application US/10264309
; Publication No. US20040022794A1
; GENERAL INFORMATION:
; APPLICANT: DURHAM, L. KATHRYN
; APPLICANT: FRIEDMAN, DAVID L.
; APPLICANT: HERATH, HERATH
; APPLICANT: KIMMEL, LIDA H.
; APPLICANT: PAREKH, RAJESH B.
; APPLICANT: POTTER, DAVID M.
; APPLICANT: ROHLFF, CHRISTIAN
; APPLICANT: SILBER, B. MICHAEL
; APPLICANT: SNYDER, PETER J.
; APPLICANT: SOARES, HOLLY D.
; APPLICANT: STIGER, THOMAS R.
; APPLICANT: SUNDERLAND, P. TREY
; APPLICANT: TOWNSEND, ROBERT R.
; APPLICANT: WHITE, W. FROST
; APPLICANT: WILLIAMS, STEPHEN A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
; TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
; FILE REFERENCE: POA-002.01
; CURRENT APPLICATION NUMBER: US/10/264,309
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: 60/326,708
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 460
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-309-460

Query Match 61.3%; Score 19; DB 15; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLKLSR 7
Db 2 TFEISR 7

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RESULT 15
US-10-601-100-105
; Sequence 105, Application US/10601100
; Publication No. US20040072261A1
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: Method for the Diagnosis and Differential Diagnosis of
; FILE REFERENCE: 11362.0038.NEUS01
; CURRENT APPLICATION NUMBER: US/10/601,100
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: EP 02447121.1
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/396,437
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 105
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-601-100-105

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Query Match      61.3%; Score 19; DB 15; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY      2 TLKLSR 7
      | :|||
Db      2 TFELSR 7

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Search completed: November 4, 2004, 01:43:17
 Job time : 69.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:42:19 ; Search time 16.6667 Seconds
(without alignments)
27.854 Million cell updates/sec

Title: US-09-712-819D-13
Perfect score: 31
Sequence: 1 LTKLSR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match	Length	ID	Description
1	29	93.5	113	3	US-08-983-607-25	Sequence 25, Appl
2	28	90.3	474	4	US-09-081-385-148	Sequence 148, Appl
3	27	87.1	127	1	US-08-482-882-45	Sequence 45, Appl
4	27	87.1	127	2	US-08-483-389-45	Sequence 45, Appl
5	27	87.1	127	2	US-08-487-113D-45	Sequence 45, Appl
6	27	87.1	127	2	US-08-473-503-45	Sequence 45, Appl
7	27	87.1	127	2	US-08-483-932-45	Sequence 45, Appl
8	27	87.1	127	2	US-08-720-420A-45	Sequence 45, Appl
9	27	87.1	127	3	US-08-714-017-45	Sequence 45, Appl
10	27	87.1	127	3	US-08-475-680-45	Sequence 45, Appl
11	27	87.1	133	4	US-09-472-087-26	Sequence 26, Appl
12	27	87.1	133	4	US-09-472-087-116	Sequence 116, Appl
13	27	87.1	141	3	US-09-134-001C-3710	Sequence 3710, Ap
14	27	87.1	221	4	US-09-252-991A-17454	Sequence 17454, A
15	27	87.1	259	4	US-09-198-452A-366	Sequence 366, App
16	27	87.1	446	4	US-09-248-796A-15638	Sequence 15638, A
17	27	87.1	551	4	US-09-538-092-738	Sequence 738, App
18	27	87.1	649	3	US-09-066-047-5	Sequence 5, Appli
19	26	83.9	70	4	US-09-543-681A-7976	Sequence 7976, Ap
20	26	83.9	172	4	US-09-248-796A-22198	Sequence 22198, A
21	26	83.9	222	4	US-09-543-681A-5317	Sequence 5317, Ap
22	26	83.9	359	3	US-09-134-001C-5618	Sequence 5618, Ap
23	26	83.9	398	4	US-10-037-616-26	Sequence 26, Appl
24	26	83.9	399	4	US-09-328-352-7463	Sequence 7463, Ap
25	26	83.9	411	4	US-09-270-767-45365	Sequence 45365, A
26	26	83.9	529	4	US-09-270-767-43463	Sequence 43463, A
27	26	83.9	695	4	US-09-543-681A-7766	Sequence 7766, Ap

28	25	80.6	32	1	US-08-477-877B-33	Sequence 33, Appl
29	25	80.6	32	1	US-07-977-696C-71	Sequence 71, Appl
30	25	80.6	32	1	US-08-129-930B-71	Sequence 71, Appl
31	25	80.6	32	2	US-08-472-281A-33	Sequence 33, Appl
32	25	80.6	32	2	US-08-477-989B-33	Sequence 33, Appl
33	25	80.6	32	3	US-08-976-288A-71	Sequence 71, Appl
34	25	80.6	32	4	US-09-563-222C-80	Sequence 80, Appl
35	25	80.6	32	4	US-09-563-222C-114	Sequence 114, App
36	25	80.6	61	4	US-09-621-976-6215	Sequence 6215, Ap
37	25	80.6	67	4	US-09-248-796A-18940	Sequence 18940, A
38	25	80.6	69	4	US-09-270-767-39121	Sequence 39121, A
39	25	80.6	69	4	US-09-270-767-54338	Sequence 54338, A
40	25	80.6	81	1	US-08-497-312-19	Sequence 19, Appl
41	25	80.6	81	4	US-09-254-180C-154	Sequence 154, App
42	25	80.6	81	4	US-09-254-180C-155	Sequence 155, App
43	25	80.6	81	4	US-09-254-180C-156	Sequence 156, App
44	25	80.6	81	4	US-09-254-180C-157	Sequence 157, App
45	25	80.6	81	4	US-09-254-180C-158	Sequence 158, App

ALIGNMENTS

RESULT 1
US-08-983-607-25
; Sequence 25, Application US/08983607
; Patent No. 6140470
; GENERAL INFORMATION:
; APPLICANT: Alan Garen
; APPLICANT: Xiaohong Cai
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; TITLE OF INVENTION: bodies
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; ADDRESSEE: and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607
; FILING DATE: April 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient immu-
; ORGANISM: nized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lymphocytes

IMMEDIATE SOURCE:
LIBRARY: DM414 scfv antibodies obtained from
LIBRARY: FUSE5 fusion phage construct
CLONE: D33
FEATURE:
NAME/KEY: light chain
OTHER INFORMATION: Xaa at position 47 is His or
OTHER INFORMATION: Gly and Xaa at position 95 is His or Gln
US-08-983-607-25

Query Match 93.5%; Score 29; DB 3; Length 113;
Best Local Similarity 85.7%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
Db 76 LTLKLSR 82

RESULT 2
US-09-081-385-148
Sequence 148, Application US/09081385
Patent No. 6593456
GENERAL INFORMATION:
APPLICANT: Gatanaga, T.
APPLICANT: Granger, G.A.
TITLE OF INVENTION: Factors Altering Tumor Necrosis
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
TITLE OF INVENTION: of Use Thereof
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/081,385
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/964,747
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wu, Frank
REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 22000-20577.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 474 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-081-385-148

Query Match 90.3%; Score 28; DB 4; Length 474;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
Db 358 LTLKLSR 364

RESULT 3
US-08-482-882-45
Sequence 45, Application US/08482882
Patent No. 5773218
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,882
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5773218and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32178
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-882-45

Query Match 87.1%; Score 27; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLSR 7
Db 92 TLKLSR 97

RESULT 4

US-08-483-389-45
; Sequence 45, Application US/08483389
; Patent No. 5811517
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-RELATED PROTEIN
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,389
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Suh, Young J.
; REGISTRATION NUMBER: P-41,337
; REFERENCE/DOCKET NUMBER: 27866/32760
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: (312) 474-6600
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-389-45
Query Match 87.1%; Score 27; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TLKLSR 7
Db 92 TLKLSR 97
RESULT 5
US-08-487-113D-45
; Sequence 45, Application US/08487113D
; Patent No. 5837822
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 120

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,113D
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,754
; FILING DATE: 05-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5837822and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32744
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-113D-45
Query Match 87.1%; Score 27; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TLKLSR 7
Db 92 TLKLSR 97
RESULT 6
US-08-473-503-45
; Sequence 45, Application US/08473503
; Patent No. 5869262
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois

```

;
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,503
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/286,754
; FILING DATE: 05-AUG-1994
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5869262and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-473-503-45

Query Match 87.1%; Score 27; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLSR 7
Db 92 TLKLSR 97

RESULT 7
US-08-483-932-45
; Sequence 45, Application US/08483932
; Patent No. 5869268
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,503
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/286,754
; FILING DATE: 05-AUG-1994
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5869262and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-932-45

Query Match 87.1%; Score 27; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLSR 7
Db 92 TLKLSR 97

RESULT 8
US-08-720-420A-45
; Sequence 45, Application US/08720420A
; Patent No. 5989843
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,420A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA:

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/ APPLICATION NUMBER: US 08/487,113
/ FILING DATE: 07-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,754
/ FILING DATE: 05-AUG-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/102,852
/ FILING DATE: 05-AUG-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/009,266
/ FILING DATE: 22-JAN-1993
/ APPLICATION NUMBER: US 07/894,061
/ FILING DATE: 05-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/889,724
/ FILING DATE: 26-MAY-1992
/ APPLICATION NUMBER: US 07/827,689
/ FILING DATE: 27-JAN-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams, Joseph A., Jr.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 33282
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 474-6300
/ TELEFAX: (312) 474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 45:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 127 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-720-420A-45

Query Match 87.1%; Score 27; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLSR 7
|||||
Db 92 TLKLSR 97

RESULT 9
US-08-714-017-45
/ Sequence 45, Application US/08/714017
/ Patent No. 6040176
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Vazeux, Rosemay
/ TITLE OF INVENTION: ICAM-Related Materials and Methods
/ NUMBER OF SEQUENCES: 116
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 6300 Sears Tower, 233 S. Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/714,017
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/286,754
/ FILING DATE:

/ APPLICATION NUMBER: US 08/102,852
/ FILING DATE: 05-AUG-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/009,266
/ FILING DATE: 22-JAN-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/894,061
/ FILING DATE: 05-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/889,724
/ FILING DATE: 26-MAY-1992
/ APPLICATION NUMBER: US 07/827,689
/ FILING DATE: 27-JAN-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 6040176and, Greta E.
/ REGISTRATION NUMBER: 35,302
/ REFERENCE/DOCKET NUMBER: 32178
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 474-6300
/ TELEFAX: (312) 474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 45:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 127 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-714-017-45

Query Match 87.1%; Score 27; DB 3; Length 127;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLSR 7
|||||
Db 92 TLKLSR 97

RESULT 10
US-08-475-680-45
/ Sequence 45, Application US/08475680
/ Patent No. 6100383
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Vazeux, Rosemay
/ TITLE OF INVENTION: ICAM-Related Materials and Methods
/ NUMBER OF SEQUENCES: 116
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 6300 Sears Tower, 233 S. Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/475,680
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/286,754
/ FILING DATE: 05-AUG-1994
/ APPLICATION NUMBER: US 08/102,852
/ FILING DATE: 05-AUG-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/009,266
/ FILING DATE: 22-JAN-1993
/ PRIOR APPLICATION DATA:

APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, EILLEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 116
LENGTH: 133
TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-116

Query Match 87.1%; Score 27; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLKLSR 7
Db 63 TLKLSR 68

RESULT 13

US-09-134-001C-3710
Sequence 3710, Application US/09134001C
Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3710
LENGTH: 141
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3710

Query Match 87.1%; Score 27; DB 3; Length 141;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTLKLSR 7
Db 53 LTMKISR 59

RESULT 14

US-09-252-991A-17454
Sequence 17454, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788

APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6100383and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32178
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-475-680-45

Query Match 87.1%; Score 27; DB 3; Length 127;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLKLSR 7
Db 92 TLKLSR 97

RESULT 11

US-09-472-087-26
Sequence 26, Application US/09472087
Patent No. 6682736

GENERAL INFORMATION:

APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, EILLEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 133
TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-26

Query Match 87.1%; Score 27; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLKLSR 7
Db 63 TLKLSR 68

RESULT 12

US-09-472-087-116
Sequence 116, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:

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; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17454
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17454

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Query Match	87.1%;	Score 27;	DB 4;	Length 221;
Best Local Similarity	85.7%;	Pred. No. 1.8e+02;		
Matches	6; Conservative	0; Mismatches	1; Indels	0; Gaps 0;

Qy 1 LTLKLSR 7
Db 161 LTFKLSR 167

RESULT 15
US-09-198-452A-366
; Sequence 366, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 366
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-366

Query Match 87.1%; Score 27; DB 4; Length 259;
Best Local Similarity 100.0%; Pred.No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLSR 7
Db 247 TLKLSR 252

Search completed: November 4, 2004, 00:54:52
Job time : 16.6667 secs

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F:130,132,158/Binding site: iron (Asp, His, Asp) #status predicted
F:158,190,240,315/Binding site: zinc (Asp, Asn, His, His) #status predicted
F:161,191,339/Active site: Asp, His, Tyr #status predicted
F:162,288/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 31; DB 1; Length 382;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
|||||
Db 73 LTLKLSR 79

RESULT 3

C71414
hypothetical protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
A:Variety: columbia
C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C:Accession: C71414
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terry, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
C.; Chalwatzis, N.
A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal
A:Reference number: A71400; MUID:98121113; PMID:9461215
A:Accession: C71414
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-555 <BEV>
A:Cross-references: UNIPROT:O23360; GB:Z97337; NID:g2244829; PID:e326846; PID:g2244863
C:Genetics:
A:Map position: 4COP9-4G3845

Query Match 93.5%; Score 29; DB 2; Length 555;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
|||||
Db 411 LTLKISR 417

RESULT 4

T33998
hypothetical protein W03G1.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 16-Aug-2004
C:Accession: T33998
R;Pauley, A.; Scheet, P.; Harper, M.
submitted to the EMBL Data Library, February 1999
A:Description: The sequence of C. elegans cosmid W03G1.
A:Reference number: Z21454
A:Accession: T33998
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-726 <PAU>
A:Cross-references: UNIPROT:Q9UAY1; EMBL:AF125964; PIDN:AAD14754.1; GSPDB:GN00022; CESP:
A:Experimental source: strain Bristol N2; clone W03G1
C:Genetics:
A:Gene: CESP:W03G1.6
A:Map position: 4
A:Introns: 21/1; 48/3; 87/3; 224/3; 280/3; 347/3; 468/3; 523/1; 584/1; 697/3
C:Superfamily: protein kinase homology

Query Match 93.5%; Score 29; DB 2; Length 726;
Best Local Similarity 85.7%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
|||||
Db 512 LTLKISR 518

RESULT 5

AE1174
hypothetical protein lmo0797 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AE1174
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1174
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-153 <GLA>
A:Cross-references: UNIPROT:Q8Y8U5; GB:NC_003210; PIDN:CAC98875.1; PID:g16410186; GSPDB:
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo0797

Query Match 90.3%; Score 28; DB 2; Length 153;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
|||||
Db 98 LTLKLSK 104

RESULT 6

AF1531
hypothetical protein lin0790 [imported] - Listeria innocua (strain Clip11262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AF1531
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AF1531
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-153 <GLA>
A:Cross-references: UNIPROT:Q92DM3; GB:AL592022; PIDN:CAC96022.1; PID:g16413241; GSPDB:
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin0790

Query Match 90.3%; Score 28; DB 2; Length 153;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
|||||
Db 98 LTLKLSK 104

RESULT 7

AE2591
DNAAK Protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AE2591
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:21608550; PMID:11743193
A;Accession: AE2591
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-633 <KUR>
A;Cross-references: UNIPROT:P50019; GB:AE008688; PIDN:AAL41147.1; PID:gl7738443; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: dnaK
A;Map position: circular chromosome
C;Superfamily: heat shock protein 70

Query Match 90.3%; Score 28; DB 2; Length 633;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTLKLSR 7
| | | | | | : |
Db 291 LTLKLTR 297

RESULT 8
E97373
dnaJ protein (heat shock protein 70) (hsp70) [imported] - Agrobacterium tumefaciens (str
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: E97373
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; PMID:21608551; PMID:11743194
A;Accession: E97373
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-633 <KUR>
A;Cross-references: UNIPROT:P50019; GB:AE007869; PIDN:AAK85942.1; PID:gl5154995; GSPDB:G
C;Genetics:
A;Gene: AGR C 195
A;Map position: circular chromosome
C;Superfamily: heat shock protein 70

Query Match 90.3%; Score 28; DB 2; Length 633;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTLKLSR 7
| | | | | | : |
Db 291 LTLKLTR 297

RESULT 9
C83734
beta-hexosamidase A precursor BH0675 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: C83734
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; PMID:20512582; PMID:11058132
A;Accession: C83734
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-686 <STO>
A;Cross-references: UNIPROT:Q9KFE22; GB:AP001509; GB:BA000004; NID:gl0173176; PIDN:BA04.
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0675

Query Match 90.3%; Score 28; DB 2; Length 686;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTLKLSR 7
| | | | | | : |
Db 471 LTLKLSR 477

RESULT 10
G82773
phage-related protein XF0705 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: G82773
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; PMID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: G82773
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-845 <SIM>
A;Cross-references: UNIPROT:Q9PFF4; GB:AE003913; GB:AE003849; NID:g9105578; PIDN:AAF835.
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer,
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins,
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasal
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF0705

Query Match 90.3%; Score 28; DB 2; Length 845;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTLKLSR 7
| | | | | | : |
Db 410 LTLKLSK 416

RESULT 11
T30212
probable transcription regulator - Staphylococcus epidermidis
C;Species: Staphylococcus epidermidis
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30212
R;Heilmann, C.; Hussain, M.; Peters, G.; Gotz, F.
Mol. Microbiol. 24, 1013-1024, 1997
A;Title: Evidence for autolysin-mediated primary attachment of Staphylococcus epidermid
A;Reference number: Z20779; PMID:97363715; PMID:9220008
A;Accession: T30212
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-139 <HEI>
A;Cross-references: UNIPROT:O33636; EMBL:U71377; NID:g2267238; PID:g2267243; PIDN:AAB63.

Query Match 87.1%; Score 27; DB 2; Length 139;
Best Local Similarity 71.4%; Pred. No. 41;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
||:|:|
Db 51 LTMKISR 57

RESULT 12
B89874
hypothetical protein SA0904 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: B89874
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: B89874
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-139 <KUR>
A;Cross-references: UNIPROT:Q99V42; GB:BA000018; PID:g13700853; PIDN:BAB42149.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA0904

Query Match 87.1%; Score 27; DB 2; Length 139;
Best Local Similarity 71.4%; Pred. No. 41;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
||:|:|
Db 51 LTMKISR 57

RESULT 13
A83573
conserved hypothetical protein PA0581 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: A83573
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bu
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83573
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-189 <STO>
A;Cross-references: UNIPROT:Q9I5V6; GB:AE004494; GB:AE004091; NID:g9946446; PIDN:AAAG0397
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA0581
C;Superfamily: Escherichia coli ygiH protein

Query Match 87.1%; Score 27; DB 2; Length 189;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
|||
Db 129 LTFKLSR 135

RESULT 14
B86937

hypothetical protein folK [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: B86937
R;Cole, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; H
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: B86937
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-191 <STO>
A;Cross-references: UNIPROT:O69528; GB:AL450380; NID:g13092570; PIDN:CAC29734.1; GSPDB:B
C;Genetics:
A;Gene: folK
C;Superfamily: 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase; 2-a

Query Match 87.1%; Score 27; DB 2; Length 191;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
|||||
Db 173 LTLKLSR 179

RESULT 15
B72089
ABC transporter, ATP-binding protein CP0412 [imported] - Chlamydomophila pneumoniae (stra
N;Alternate names: rRNA methylase
C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 16-Aug-2004
C;Accession: B72089; H81580
R;Kelman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: B72089
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-259 <ARN>
A;Cross-references: UNIPROT:Q9Z8J5; GB:AE001619; GB:AE001363; NID:g4376620; PIDN:AAD184
A;Experimental source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: H81580
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-259 <REA>
A;Cross-references: GB:AE002202; GB:AE002161; NID:g7189324; PIDN:AAF38256.1; PID:g71893
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: ytgB 1; CP0412
C;Superfamily: ATP-binding cassette homology
F;24-217/Domain: ATP-binding cassette homology <ABC>

Query Match 87.1%; Score 27; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLSR 7
|||||
Db 247 TLKLSR 252

Search completed: November 4, 2004, 00:48:42
Job time : 20 secs

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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:41:09 ; Search time 103 Seconds
(without alignments)
39.103 Million cell updates/sec

Title: US-09-712-819D-13
Perfect score: 31
Sequence: 1 LTKLSR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	31	100.0	203	1 YGIM_HAEIN	P42722 haemophilus
2	29	93.5	367	2 Q986H5	Q986h5 rhizobium 1
3	29	93.5	459	2 Q6NI26	Q6ni26 corynebacte
4	29	93.5	459	2 CAE49472	CAE49472 corynebac
5	29	93.5	465	2 Q7NT21	Q7nt21 chromobacte
6	29	93.5	526	2 Q9LG01	Q9lg01 arabidopsis
7	29	93.5	555	2 O23360	O23360 arabidopsis
8	29	93.5	636	2 Q74H59	Q74h59 geobacter s
9	29	93.5	636	2 AAR33368	AAR33368 geobacter
10	29	93.5	641	1 DNAK_RHIME	P42374 rhizobium m
11	29	93.5	679	2 Q7SEB7	Q7seb7 neurospora
12	29	93.5	722	2 Q86FM0	Q86fm0 caenorhabdi
13	29	93.5	726	2 Q9UAY1	Q9uay1 caenorhabdi
14	29	93.5	903	2 Q9VUM8	Q9vum8 drosophila
15	29	93.5	971	2 Q7KUM3	Q7kum3 drosophila
16	29	93.5	971	2 AAS65000	AAS65000 drosophil
17	28	90.3	153	2 Q92DM3	Q92dm3 listeria in
18	28	90.3	153	2 Q8Y8U5	Q8y8u5 listeria mo
19	28	90.3	153	2 Q722C0	Q722c0 listeria mo
20	28	90.3	153	2 AAT03594	AAT03594 listeria
21	28	90.3	296	2 Q72R88	Q72r88 leptospira
22	28	90.3	296	2 Q8F4I7	Q8f4i7 leptospira
23	28	90.3	296	2 AAS70446	AAS70446 leptospir
24	28	90.3	308	2 Q86DE4	Q86de4 heterodera
25	28	90.3	309	2 Q6MH57	Q6mh57 bdellovibri
26	28	90.3	309	2 CAE81070	CAE81070 brachydanio
27	28	90.3	316	2 Q90428	Q90428 brachydanio
28	28	90.3	569	2 Q88FI3	Q88fi3 pseudomonas
29	28	90.3	633	1 DNAK_AGR75	P50019 agrobacteri
30	28	90.3	634	2 Q6RSN6	Q6rsn6 agrobacteri
31	28	90.3	634	2 AAR84665	AAR84665 agrobacte

32	28	90.3	638	1 DNAK_RHILE	O33528 rhizobium 1
33	28	90.3	638	1 DNAK_RHILO	Q98dd1 rhizobium 1
34	28	90.3	686	2 Q9KF22	Q9kf22 bacillus ha
35	28	90.3	845	2 Q9PFF4	Q9pff4 xylella fas
36	28	90.3	969	2 BAC86701	BAC86701 homo sapi
37	28	90.3	1424	2 Q75DK8	Q75dk8 ashbya goss
38	28	90.3	1424	2 AAS50783	AAS50783 ashbya go
39	28	90.3	1522	1 ARHB_HUMAN	O15085 homo sapien
40	28	90.3	1562	2 Q6PEW2	Q6pew2 homo sapien
41	28	90.3	1562	2 AAH57394	AAH57394 homo sapi
42	28	90.3	2691	2 CAG26692	CAG26692 mus muscu
43	28	90.3	2697	2 CAG26691	CAG26691 homo sapi
44	28	90.3	2798	1 NPBL_MOUSE	Q6kcd5 mus musculu
45	28	90.3	2798	2 CAF25291	CAF25291 mus muscu

ALIGNMENTS

RESULT 1

ID	YGIM_HAEIN	STANDARD;	PRT;	203 AA.
AC	P44272;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Hypothetical protein H11605 precursor.			
GN	OrderedLocusNames=H11605;			
OS	Haemophilus influenzae.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;			
OC	Pasteurellaceae; Haemophilus.			
OX	NCBI_TaxID=727;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Rd / KW20 / ATCC 51907;			
RA	MEDLINE=95350630; PubMed=7542800;			
RA	Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,			
RA	Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,			
RA	McKenney K., Sutton G.G., FitzHugh W., Fields C.A., Gocayne J.D.,			
RA	Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,			
RA	Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,			
RA	Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,			
RA	Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,			
RA	Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,			
RA	Venter J.C.;			
RT	"Whole-genome random sequencing and assembly of Haemophilus influenzae			
RL	Rd.";			
CC	Science 269:496-512(1995).			
CC	-!- SIMILARITY: Strong, to E.coli ygim.			

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EMBL; U32834; AAC23249.1; -.	
PIR; C64038; C64038.	
TIGR; H11605; -.	
InterPro; IPR003646; SH3_bac.	
SMART; SM00287; SH3b; 1.	
Complete proteome; Hypothetical protein; Signal; Transmembrane.	
SIGNAL	1 23 Potential.
CHAIN	24 203 Hypothetical protein H11605.
TRANSMEM	167 189 Potential.
SEQUENCE	203 AA; 23112 MW; FAFC5E229FD29C05 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 203;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```

RESULT 5
Q7NT21
ID Q7NT21 PRELIMINARY; PRT; 465 AA.
AC Q7NT21;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Transmembrane multidrug resistance efflux protein.
GN Name=ebrB; OrderedLocusNames=CV3243;
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxID=536;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12472 / DSM 30191;
RX MEDLINE=22882880; PubMed=14500782;
RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,
RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA Carvalho C.M.B., Cascado J.C.M., Cavada B.S., Chueire L.M.O.,
RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
RA Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,
RA di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA Santos E.B.P., Santos F.R., Schneider M.P.C., Senanez H.N.,
RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
RA Vettore A., Wasseem R., Zaha A., Simpson A.J.G.;
RT "The complete genome sequence of Chromobacterium violaceum reveals
RT remarkable and exploitable bacterial adaptability."
RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
DR EMBL; AE016921; AAQ60908.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR PROSITE; PS50850; MFS; 1.
DR Complete proteome; Transmembrane.
KW SEQUENCE 465 AA; 46835 MW; 8332FE3DDDC56E2E CRC64;

Query Match 93.5%; Score 29; DB 2; Length 465;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LITLKLRS 7
Db 379 LITLKLRS 385

RESULT 6
Q9LG01
ID Q9LG01 PRELIMINARY; PRT; 526 AA.
AC Q9LG01;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE F2ON2.9.

Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C.,
RA Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Shinn P.P., Buehler E.E., Dunn P.P., Feng J.J., Kim C.C., Li Y.Y.,
RA Walker M.M., Altafi H.H., Araujo R.R., Conn L.L., Conway A.A.B.,
RA Gonzalez A.A., Hansen N.N.F., Huizar L.L., Kremenetskaia I.I.,
RA Lenz C.C., Li J.J., Liu S.S., Lueros S.S., Rowley D.D., Schwartz J.J.,
RA Toriumi M.M., Vysotskaia V.V., Yu G.G., Davis R.R.W.,
RA Federspiel N.N.A., Theologis A.A., Ecker J.J.R.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howng B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EMBL; AC002328; AAF79496.1; -
DR InterPro; IPR001810; F-box.
DR InterPro; IPR006566; FBD.
DR InterPro; IPR008945; Skp1_Skp2.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00579; FBD; 1.
DR SMART; SM00256; FBOX; 1.
DR PROSITE; PS50181; FBOX; 1.
SQ SEQUENCE 526 AA; 60437 MW; 6C45C35BED85B749 CRC64;

Query Match 93.5%; Score 29; DB 2; Length 526;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LITLKLRS 7
Db 294 LITLKLRS 300

RESULT 7
Q23360
ID Q23360 PRELIMINARY; PRT; 555 AA.
AC Q23360;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein AT4G15060.
GN Name=AT4G15060; Synonym=AT4G15060;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98121113; PubMed=9461215;
RA Bevan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,
RA Bergkamp R., Dirkse W., van Staveren M., Stiekema W., Drost L.,
RA Ridley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler H.,

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DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
SQ SEQUENCE 636 AA; 68467 MW; 1519C2E3B6A380A4 CRC64;

Query Match 93.5%; Score 29; DB 2; Length 636;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
|:|:|:|
Db 291 LTMKLSR 297

RESULT 9
AAR33368 PRELIMINARY; PRT; 636 AA.
ID AAR33368
AC AAR33368;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Chapterone protein dnaK.
GN DNaK OR GSU0033.
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI_TaxID=35554;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304;
RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu D., Ward N.L., Beanan M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Daviden T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weidman J., Khouri H.M., Feldblyum T.V., Utterback T.R.,
RA Van Aken S.E., Lovley D.R., Fraser C.M.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments.";
RL Science 302:1967-1969(2003).
DR EMBL; AE017207; AAR33368.1; -.
DR TIGR; GSU0033; -.
SQ SEQUENCE 636 AA; 68467 MW; 1519C2E3B6A380A4 CRC64;

Query Match 93.5%; Score 29; DB 2; Length 636;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
|:|:|:|
Db 291 LTMKLSR 297

RESULT 10
DNaK RHIME STANDARD; PRT; 641 AA.
ID DNaK RHIME
AC P42374;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chapterone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa
DE protein) (Hsp70).
GN Name=dnaK; OrderedLocusNames=P00182; ORFNames=SMC02857;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25416;
RX MEDLINE=95095949; PubMed=7528198;
RA Falah M., Gupta R.S.;
RT "Cloning of the hsp70 (dnaK) genes from Rhizobium meliloti and

RA Wedler E., Wambutt R., Weitzeneegger T., Pohl T.M., Terryn N.,
RA Gielen J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,
RA Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kotter P.,
RA Entian K.D., Rieger M., Schaeffer M., Funk B., Mueller-Auer S.,
RA Silvey M., James R., Montfort A., Pons A., Puigdomenech P., Douka A.,
RA Voukelatou E., Milioni D., Hatzopoulos P., Piravandi E., Obermaier B.,
RA Hilbert H., Duesterhoft A., Moores T., Jones J.D.G., Eneva T.,
RA Palme K., Benes V., Rechman S., Ansoorge W., Cooke R., Berger C.,
RA Delseny M., Voet M., Volckaert G., Mewes H.W., Klosterman S.,
RA Schueller C., Chalmatzis N.;
RT "Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of
RT Arabidopsis thaliana.";
RL Nature 391:485-488(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z97337; CAB10285.1; -.
DR EMBL; AL161540; CAB78548.1; -.
DR PIR; C71414; C71414.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR006566; FBD.
DR InterPro; IPR008945; Skp1_Skp2.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00579; FBD; 1.
KW Hypothetical protein.
SQ SEQUENCE 555 AA; 64199 MW; C8D02D8C05481FFB CRC64;

Query Match 93.5%; Score 29; DB 2; Length 555;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
|:|:|:|
Db 411 LTLKISR 417

RESULT 8
Q74H59 PRELIMINARY; PRT; 636 AA.
ID Q74H59
AC Q74H59;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Chapterone protein dnaK.
GN Name=dnaK; ORFNames=GSU0033;
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI_TaxID=35554;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304; DOI=10.1126/science.1088727;
RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu D., Ward N.L., Beanan M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Daviden T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,
RA Van Aken S.E., Lovley D.R., Fraser C.M.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments.";
RL Science 302:1967-1969(2003).
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AE017180; AAR33368.1; -.
DR TIGR; GSU0033; -.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.

RT Pseudomonas cepacia: phylogenetic analyses of mitochondrial origin
RT based on a highly conserved protein sequence.";
RL J. Bacteriol. 176:7748-7753(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Fumelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
RN [3]
RP SEQUENCE OF 1-101 FROM N.A.
RC STRAIN=104A14;
RX MEDLINE=99022212; PubMed=9805396;
RA Summers M.L., Elkins J.G., Elliott B.A., McDermott T.R.;
RT "Expression and regulation of phosphate stress inducible genes in
RT Sinorhizobium meliloti.";
RL Mol. Plant Microbe Interact. 11:1094-1101(1998).
CC -!- FUNCTION: Acts as a chaperone (By similarity).
CC -!- INDUCTION: By stress conditions e.g. heat shock (By similarity).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L36602; AAA64925.1; -;
DR EMBL; AL591782; CAC41569.1; -;
DR EMBL; AF074451; AAD42995.1; -;
DR HSP; P04475; 1DG4.
DR HAMAP; MF_00332; -; 1.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR TIGRfam; TIGR01991; Hsca; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Complete proteome; Heat shock;
KW Phosphorylation.
FT MOD_RES 198 198 Phosphothreonine (by autocatalysis) (By
FT similarity).
FT CONFLICT 405 405 R -> V (in Ref. 1).
FT CONFLICT 570 570 A -> R (in Ref. 1).
FT CONFLICT 611 614 DAAA -> MPPP (in Ref. 1).
SQ SEQUENCE 641 AA; 68949 MW; B711D9BD9CC2360C CRC64;

Query Match 93.5%; Score 29; DB 1; Length 641;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
Db 291 LTMKLSR 297

RESULT 11
Q7SEB7 ID Q7SEB7 PRELIMINARY; PRT; 679 AA.
AC Q7SEB7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Predicted protein.
GN Name=NCU00817.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamvysselis M., Mauceli E., Biele C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AABX0100035; EAA35124.1; -;
SQ SEQUENCE 679 AA; 72117 MW; D83AEF7E01292FE8 CRC64;

Query Match 93.5%; Score 29; DB 2; Length 679;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
Db 176 LTIKLSR 182

RESULT 12
Q86FM0 ID Q86FM0 PRELIMINARY; PRT; 722 AA.
AC Q86FM0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein W03G1.6.
GN Name=W03G1.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Wilson R.;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Pauley A., Scheet P., Harper M.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.

RC	STRAIN=Bristol N2;	DR	GO; GO:0016740; F:transferase activity; IEA.
RA	Wilson R.;	DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
RL	Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.	DR	InterPro; IPR001772; Kinase Cterm.
DR	EMBL; AF125964; AAP13765.1; -.	DR	InterPro; IPR011009; Kinase_like.
DR	HSSP; P31751; 1GZK.	DR	InterPro; IPR000719; Prot_kinase.
DR	GO; GO:0005524; F:ATP binding; IEA.	DR	InterPro; IPR002290; Ser_thr_pkinase.
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.	DR	InterPro; IPR008271; Ser_thr_pkin_AS.
DR	GO; GO:0016740; F:transferase activity; IEA.	DR	Pfam; PF02149; KAI; 1.
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.	DR	Pfam; PF00069; Pkinase; 1.
DR	InterPro; IPR011009; Kinase_like.	DR	SMART; SM00220; S_TKC; 1.
DR	InterPro; IPR000719; Prot_kinase.	DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	InterPro; IPR002290; Ser_thr_pkinase.	DR	PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR	InterPro; IPR008271; Ser_thr_pkin_AS.	DR	PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN 1.
DR	Pfam; PF00069; Pkinase; 1.	KW	ATP-binding; Hypothetical protein; Kinase; Transferase.
DR	ProDom; PD000001; Prot_kinase; 1.	SQ	SEQUENCE 726 AA; 82649 MW; FCBD08345D58213B CRC64;
DR	SMART; SM00220; S_TKC; 1.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.		
DR	PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.		
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN 1.		
KW	ATP-binding; Hypothetical protein; Kinase; Transferase.		
SQ	SEQUENCE 722 AA; 82249 MW; C3C3B2AB5CED6FB8 CRC64;		
	Query Match 93.5%; Score 29; DB 2; Length 722;		
	Best Local Similarity 85.7%; Pred. No. 2.8e+02;		
	Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
QY	1 LTLKLSR 7		
	:		
Db	512 LTLKISR 518		
	RESULT 13		
Q9UAY1			
ID	Q9UAY1 PRELIMINARY; PRT; 726 AA.		
AC	Q9UAY1;		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Hypothetical protein W03G1.6.		
GN	ORFNames=W03G1.6;		
OS	Caenorhabditis elegans.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;		
OC	Rhabditidae; Peloderinae; Caenorhabditis.		
OX	NCBI_TaxID=6239;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Bristol N2;		
RX	MEDLINE=99069613; PubMed=9851916;		
RA	Wilson R.;		
RT	"Genome sequence of the nematode C. elegans: a platform for		
RT	investigating biology. The C. elegans Sequencing Consortium.";		
RL	Science 282:2012-2018(1998).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Bristol N2;		
RA	Pauley A., Scheet P., Harper M.;		
RL	Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Bristol N2;		
RA	Waterston R.;		
RL	Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Bristol N2;		
RA	Wilson R.;		
RL	Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; AF125964; AAD14754.1; -.		
DR	PIR; T33998; T33998.		
DR	HSSP; Q63450; 1A06.		
DR	WormPep; W03G1.6; CE17284.		
DR	GO; GO:0005524; F:ATP binding; IEA.		
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.		
DR			

DR	GO; GO:0016740; F:transferase activity; IEA.
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR	InterPro; IPR001772; Kinase Cterm.
DR	InterPro; IPR011009; Kinase_like.
DR	InterPro; IPR000719; Prot_kinase.
DR	InterPro; IPR002290; Ser_thr_pkinase.
DR	InterPro; IPR008271; Ser_thr_pkin_AS.
DR	Pfam; PF02149; KAI; 1.
DR	Pfam; PF00069; Pkinase; 1.
DR	SMART; SM00220; S_TKC; 1.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN 1.
KW	ATP-binding; Hypothetical protein; Kinase; Transferase.
SQ	SEQUENCE 726 AA; 82649 MW; FCBD08345D58213B CRC64;
	Query Match 93.5%; Score 29; DB 2; Length 726;
	Best Local Similarity 85.7%; Pred. No. 2.9e+02;
	Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 LTLKLSR 7
	:
Db	512 LTLKISR 518
	RESULT 14
Q9VUM8	
ID	Q9VUM8 PRELIMINARY; PRT; 903 AA.
AC	Q9VUM8;
DT	01-MAY-2000 (TrEMBLrel. 13, Created)
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	CG7255-PB (Cg7255-pa).
GN	ORFNames=CG7255;
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA	Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA	Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA	Balleg R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA	Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA	Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA	Lasko P., Lei Y., Levitsky A., Li J., Li Z., Liang Y., Lin X.,
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA	Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirska R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirska R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a Genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FLYBASE;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FLYBASE;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003531; AAF49646.2; -;
DR FlyBase; FBgn0036493; CG7255;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
KW Transmembrane; Transport.
SQ SEQUENCE 903 AA; 99174 MW; DBADA5FED68D7BC5 CRC64;

Query Match 93.5%; Score 29; DB 2; Length 903;
Best Local Similarity 85.7%; Pred. No. 3.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTKLSR 7
Db :|||||
596 ITLKLRSR 602

RESULT 15
Q7KUM3
ID Q7KUM3 PRELIMINARY; PRT; 971 AA.

AC Q7KUM3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CG7255-PD (CG7255-pe).
GN ORFNames=CG7255;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brattier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
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RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirska R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
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RN [3]
RP SEQUENCE FROM N.A.
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RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirska R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a Genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

[4]
RN SEQUENCE FROM N.A.
RP MEDLINE=22426069; PubMed=12537572;
RX Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celisner S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FLYBASE;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FLYBASE;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003531; AAS6500.1; -;
DR InterPro; IPR002293; AA/rel_permeasel.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
KW Transmembrane; Transport.
SQ SEQUENCE 971 AA; 106747 MW; 919608FD06398DF0 CRC64;

Query Match 93.5%; Score 29; DB 2; Length 971;
Best Local Similarity 85.7%; Pred. No. 3.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTLKLSR 7
Db 664 ITLKLSR 670

Search completed: November 4, 2004, 00:53:59
Job time : 105 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:33:03 ; Search time 60 Seconds
(without alignments)
41.852 Million cell updates/sec

Title: US-09-712-819D-13
Perfect score: 31
Sequence: 1 LTLKLSR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	29	93.5	113	2	AAW13517
2	29	93.5	131	2	AAR20065
3	29	93.5	638	8	ADJ49770
4	29	93.5	641	8	ADJ49389
5	29	93.5	641	8	ADJ50245
6	29	93.5	870	4	ABB66159
7	29	93.5	880	4	ABB63131
8	28	90.3	153	5	ABB49428
9	28	90.3	155	4	AAG72986
10	28	90.3	212	4	AAB90806
11	28	90.3	374	3	AAB42328
12	28	90.3	474	3	AAJ56509
13	28	90.3	633	8	ADJ49412
14	28	90.3	638	8	ADJ49826
15	28	90.3	638	8	ADJ49161
16	28	90.3	1520	2	AAJ41010
17	28	90.3	1522	8	ADF45494
18	28	90.3	1522	8	ADH23366
19	28	90.3	1522	8	ADQ17442
20	28	90.3	1562	8	ADF45522
21	28	90.3	1562	8	ADF45496
22	28	90.3	1736	7	ADE08492
23	28	90.3	2685	7	ADC06796
24	28	90.3	2804	8	ADN04576
25	27	87.1	31	6	ABO04917

26	27	87.1	127	2	AAW71254	Aaw71254 Murine an
27	27	87.1	127	2	AAW76124	Aaw76124 Murine IC
28	27	87.1	127	2	AAW81448	Aaw81448 Murine an
29	27	87.1	127	2	AAW00781	Aay00781 Antibody
30	27	87.1	127	3	AAJ50751	Aay50751 Murine an
31	27	87.1	127	3	AAJ3044	Aab13044 Murine IC
32	27	87.1	127	3	AAJ82443	Aay82443 Murine an
33	27	87.1	127	5	AAU70936	Aau70936 Murine mo
34	27	87.1	127	7	ADG25695	Adg25695 Mouse ant
35	27	87.1	133	3	AAJ93726	Aay93726 The kappa
36	27	87.1	133	6	AAE35910	Aae35910 Human 12.
37	27	87.1	139	6	ABM73321	Abm73321 Staphyloc
38	27	87.1	141	5	ABP38865	Abp38865 Staphyloc
39	27	87.1	189	4	AAU36206	Aau36206 Pseudomon
40	27	87.1	189	6	ABU38277	Abu38277 Protein e
41	27	87.1	191	6	ABU35748	Abu35748 Protein e
42	27	87.1	193	4	AAU52716	Aau52716 Propionib
43	27	87.1	193	6	ABM49235	Abm49235 Propionib
44	27	87.1	221	7	ABO68708	Abo68708 Pseudomon
45	27	87.1	239	3	AAJ82611	Aay82611 Human PTH

ALIGNMENTS

RESULT 1
AAW13517
ID AAW13517 standard; protein; 113 AA.
XX
AC AAW13517;
XX
DT 28-OCT-1997 (first entry)
XX
DE Anti-melanoma light chain antibody clone D33.
XX
KW Human; monoclonal antitumour antibody; peripheral blood lymphocyte;
KW cancer; tumourigenesis; anticancer vaccine.
XX Homo sapiens.

Key	Location/Qualifiers
Region	24..39
Misc-difference	/label= CDR1
Region	/label= His, Gly
Region	55..61
Misc-difference	/label= CDR2
Region	94..102
Misc-difference	/label= CDR3
Misc-difference	/label= His, Gln
W09702479-A2.	
23-JAN-1997.	
28-JUN-1996;	96WO-IB001032.
30-JUN-1995;	95US-00497647.
(UYVA) UNIV YALE.	
Garen A, Cai X;	
WPI; 1997-109061/10.	

Prod. of human monoclonal anti-tumour antibodies - by screening a fusion
phage library produced using peripheral blood lymphocytes from a cancer
patient.
Claim 19; Page 55; 82pp; English.
A process for isolating and synthesising human monoclonal anti-tumour

antibodies has been produced. The process involves: (a) constructing at least one fusion phage library from the peripheral blood lymphocytes (PBLs) of a cancer patient; (b) screening for anti-tumour antibodies in the phage library in a binding assay with cultured tumour cells of the same type as the patient's tumour; (c) removing extraneous antibodies by absorption against normal human cells; (d) cloning the phage selected in step (b) and (c); (e) assaying the specificity of the cloned phage by incubating the phage with at least two types of cultured normal cells; and (f) further testing the specificity of cloned phage that do not bind to either cell line of cultured normal cells in further binding assays to cultured tumour cells derived from more than one other tumour that is not the patient's tumour. The present sequence represents a human light chain antibody, from an scFv antibody fusion phage library, produced by a method as described above. The antibodies produced can be used for diagnostic and therapeutic applications and for isolating tumour antigens for studying tumourigenesis or for use as anti-cancer vaccines. The human antibodies have low immunogenicity in humans compared to murine monoclonal antibodies (MAbs). Since the antibodies are isolated from fusion phage libraries, their affinity and specificity for a tumour cell line can be improved by genetic manipulations

Query Match 93.5%; Score 29; DB 2; Length 113;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
| | | | : | |
Db 76 LTLKISR 82

RESULT 2
AAR20065
ID AAR20065 standard; protein; 131 AA.

XX AAR20065;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 27-MAR-1992 (first entry)
XX
DE MRK16-L chain.
XX
KW Monoclonal antibody; light; heavy; chain; cancer; drug resistance.
XX
OS Homo; sapiens.
OS Mus musculus.
OS Chimeric.

XX JP03254691-A.
XX
PD 13-NOV-1991.
XX
PF 02-MAR-1990; 90JP-00051563.
XX
PR 02-MAR-1990; 90JP-00051563.
XX
PA (GANK-) ZH GAN KENYUKAI.
PA (FUJI-) FUJITA GAKUEN GH.
PA (NICA-) JAPAN FOUND CANCER RES.
XX
DR WPI; 1992-002461/01.
DR N-PSDB; AAQ20071.
XX
PT Chimera antibody against drug resistant cancer - comprises variable region homologous to region in mouse monoclonal antibody and constant region homologous to region in human immunoglobulin.

XX Disclosure; Fig 5; 20pp; Japanese.
XX
CC A chimeric antibody against drug-resistant cancer consists of (1) a variable region having an amino acid sequence homologous to a variable

CC region in the mouse monoclonal antibody against drug- resistance and (2)
CC a constant region having an amino acid sequence homologous to the
CC constant region in human immunoglobulin. The chimeric antibody
CC selectively inhibits the growth of cancer cells showing drug resistance
CC or enhances the sensitivity to the drug. The antibody is very low in
CC immunogenicity. The MRK16-H chain is shown in AAQ20070. (Updated on 25-
CC MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS
CC field)

XX Sequence 131 AA;
SQ
Query Match 93.5%; Score 29; DB 2; Length 131;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
| | | | : | |
Db 95 LTLKISR 101

RESULT 3
ADJ49770
ID ADJ49770 standard; protein; 638 AA.

XX ADJ49770;
AC
XX
DT 06-MAY-2004 (first entry)
XX
DE Oil-associated gene related protein #1270.
XX
KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
XX
OS Unidentified.

XX US2004025202-A1.
XX
PD 05-FEB-2004.
XX
PF 14-MAR-2003; 2003US-00389566.
XX
PR 15-MAR-2002; 2002US-0365301P.
PR 26-JUN-2002; 2002US-0391786P.
PR 26-JUN-2002; 2002US-0392018P.

XX (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.

XX Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
PI WPI; 2004-142683/14.
XX
PT Novel recombinant DNA construct comprising a promoter functional in
PT plants operably linked to an oil-associated gene for producing transgenic
PT plant seed.

XX Example 3; SEQ ID NO 1774; 22pp; English.
XX
PS The invention relates to a recombinant DNA construct comprising a
CC promoter functional in plants operably linked to an oil-associated gene.
CC The construct is useful for transgenic plant seed which has in its genome
CC the construct, that is functional in the plant to transcribe the oil-
CC associated gene. The transgenic plant seed grows into a plant having
CC enhanced seed oil as compared to wild type. The construct is useful for
CC producing hybrid maize seed. The transgenic plant seed is useful for
CC producing vegetable oil. The present sequence represents the amino acid
CC sequence of an oil-associated gene related protein.

XX Sequence 638 AA;

Query Match 93.5%; Score 29; DB 8; Length 638;

RESULT 5
ADJ50245
ID ADJ50245 standard; protein; 641 AA.
XX

XX PD 27-SEP-2001.
 XX XX
 PF 23-MAR-2001; 2001WO-US009231.
 XX XX
 PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX XX
 PA (PEKE) PE CORP NY.
 XX XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL10262.
 XX XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX XX
 PS Disclosure; SEQ ID NO 25269; 21pp + Sequence Listing; English.
 XX XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX XX
 SQ Sequence 870 AA;
 Query Match 93.5%; Score 29; DB 4; Length 870;
 Best Local Similarity 85.7%; Pred. No. 9.6e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LTLKLSR 7
 Db :|||||
 563 ITLKLSR 569
 RESULT 7
 ABB63131
 ID ABB63131 standard; protein; 880 AA.
 XX AC ABB63131;
 XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 16185.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 XX pharmaceutical.
 XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PE 23-MAR-2001; 2001WO-US009231.
 XX PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX XX
 PA (PEKE) PE CORP NY.
 XX XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL07234.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX XX
 PS Disclosure; SEQ ID NO 16185; 21pp + Sequence Listing; English.
 XX XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX XX
 SQ Sequence 880 AA;
 Query Match 93.5%; Score 29; DB 4; Length 880;
 Best Local Similarity 85.7%; Pred. No. 9.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LTLKLSR 7
 Db :|||||
 573 ITLKLSR 579
 RESULT 8
 ABB49428
 ID ABB49428 standard; protein; 153 AA.
 XX AC ABB49428;
 XX DT 05-FEB-2002 (first entry)
 XX DE Listeria monocytogenes protein #2132.
 XX KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
 KW vitamin B12; bacterial infection; disease.
 XX OS Listeria monocytogenes.
 XX PN WO200177335-A2.
 XX PD 18-OCT-2001.
 XX PF 11-APR-2001; 2001WO-FR001118.
 XX PR 11-APR-2000; 2000FR-00004629.
 XX PA (INSP) INST PASTEUR.
 XX PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
 PI Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
 PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
 PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
 PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
 PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
 PI Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
 PI Rose M, Voss H;
 XX XX
 DR WPI; 2002-010914/01.
 XX XX
 PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
 PT and prevention of Listeria and related bacterial infections, and related
 PT polypeptides.
 XX XX
 PS Claim 6; SEQ ID NO 2133; 192pp; French.
 XX XX
 CC The present invention relates to the genome sequence of Listeria
 CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of

CC it are useful for selecting probes and primers for detecting genes in L.
CC monocytes and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of L. monocytes and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate L. monocytes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by L.
CC monocytes and related organisms. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 153 AA;

Query Match 90.3%; Score 28; DB 5; Length 153;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTLKLSR 7
Db 98 LTLKLSK 104

RESULT 9
AAG72986
ID AAG72986 standard; protein; 155 AA.

XX AAG72986;

DT 30-JUL-2001 (first entry)

DE Olfactory receptor-like polypeptide, SEQ ID NO: 2668.

XX Human; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation.

XX Unidentified.

PN WO200127158-A2.

XX 19-APR-2001.

PF 06-OCT-2000; 2000WO-US027582.

XX 08-OCT-1999; 99US-0158615P.

PR 24-FEB-2000; 2000US-0184809P.

XX (DIGI-) DIGISCENTS.

PA (YEDA) YEDA RES & DEV CO LTD.

XX Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

PI WPI; 2001-290713/30.

XX New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists.

PS Example 6; Page 1804; 1857pp; English.

XX The present sequence is an olfactory receptor polypeptide which was used
CC as a query sequence in a database search of olfactory receptor (OR)-like
CC sequences. The invention relates to isolated polynucleotides encoding
CC polypeptides involved in olfactory sensation. The polynucleotides can be
CC used in screening for olfactory agonists and antagonists. The methods
CC allow for the determination of primary scents and the identification of
CC the odour receptors used to detect these primary scents. The methods also
CC enable determination of secondary scents and the identification of

CC combinations of odour receptors that are involved in detecting such
CC secondary scents. This enables the construction of a scent representation
CC (also called a scent fingerprint or scent profile), which may be used to
CC re-create and edit scents. Libraries of olfactory receptors are useful
CC for determining the interaction pattern of a composition with the
CC receptors, and can be used for determining differences in the olfactory
CC faculties of different individuals
XX
SQ Sequence 155 AA;

Query Match 90.3%; Score 28; DB 4; Length 155;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTLKLSR 7
Db 35 LTLRLSR 41

RESULT 10
AAB90806
ID AAB90806 standard; protein; 212 AA.

XX AAB90806;

DT 15-JUN-2001 (first entry)

DE Human shear stress-response protein SEQ ID NO: 112.

XX Human; shear stress-response protein; vascular disease; arteriosclerosis.

OS Homo sapiens.

PN WO200125427-A1.

XX 12-APR-2001.

PF 02-OCT-2000; 2000WO-JP006840.

XX 01-OCT-1999; 99JP-00280976.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PA (NOJI/) NOJIMA H.

XX Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;

PI Kuga T, Sekine S, Nakamura Y, Sugano S;

XX WPI; 2001-266308/27.

DR N-PSDB; AAH02929.

XX DNA sequences, proteins encoded by them and antibodies against them
PT useful in diagnosis and treatment of vascular disease caused by
PT arteriosclerosis.

PS Claim 52; Page 551-552; 678pp; Japanese.

XX The present invention provides the protein and coding sequences of a
CC number of human shear stress response proteins. These are useful in the
CC diagnosis, treatment and screening of vascular diseases caused by
CC arteriosclerosis, including heart failure, post-PRCA restenosis and
CC hypertension

XX Sequence 212 AA;

Query Match 90.3%; Score 28; DB 4; Length 212;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTLKLSR 7
Db 200 LTLKLSK 206

RESULT 11
AAB42328
ID AAB42328 standard; protein; 374 AA.
XX
AC AAB42328;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human ORFX ORF2092 polypeptide sequence SEQ ID NO:4184.
XX
KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive.
XX
OS Homo sapiens.
XX
PN WO200058473-A2.
XX
PD 05-OCT-2000.
XX
PF 31-MAR-2000; 2000WO-US008621.
XX
PR 31-MAR-1999; 99US-0127607P.
PR 02-APR-1999; 99US-0127636P.
PR 05-APR-1999; 99US-0127728P.
PR 30-MAR-2000; 2000US-00540763.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
PI WPI; 2000-602362/57.
XX N-PSDB; AAC76537.
DR
DR Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease.
XX
PS Claim 11; Page 3376-3377; 5507pp; English.
XX
CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
CC dermatological; immunosuppressive; antiinflammatory; antibacterial;
CC antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
CC sequences can be used for determining the presence of or predisposition
CC to, or preventing or treating pathological conditions associated with an
CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
CC proteins in gene therapy vectors. The proteins and nucleic acids may be
CC used to treat cancers, proliferative disorders, neurodegenerative
CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
CC storage, systemic lupus erythematosus, severe combined immunodeficiency
CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
CC enhance coagulation; to inhibit thrombosis; and as a contraceptive
XX
SQ Sequence 374 AA;

Query Match 90.3%; Score 28; DB 3; Length 374;
Best Local Similarity 85.7%; Pred. No. 6.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LTLKLSR 7
Db 226 LTLRLSR 232
RESULT 12
AAY56509
ID AAY56509 standard; protein; 474 AA.
XX
AC AAY56509;
XX
DT 17-FEB-2000 (first entry)
XX
DE Human Jurkat cell clone 2-9 AIM2 complementary strand ORF protein.
XX
KW Human; Jurkat cell; tumour necrosis factor receptor releasing enzyme;
KW TRRE; cytokine; TNF; identification; cytostatic; anti-inflammatory;
KW cardiant; immunomodulator; antiarthritic; antibacterial; cancer;
KW heart failure; cachexia; inflammation; endotoxin shock; arthritis;
KW multiple sclerosis; sepsis.
XX
OS Homo sapiens.
XX
PN WO9958559-A2.
XX
PD 18-NOV-1999.
XX
PF 14-MAY-1999; 99WO-US010793.
XX
PR 14-MAY-1998; 98US-00081385.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Gatanaga T, Granger GA;
XX
DR WPI; 2000-039067/03.
DR N-PSDB; AAZ38863.
XX
PT Tumour necrosis factor receptor releasing enzyme modulators and
PT polynucleotides.
XX
PS Example 5; Page 96-97; 106pp; English.
XX
CC The present invention describes isolated polynucleotides (A) comprising a
CC sequence expressed at the mRNA level in Jurkat T cells and showing
CC increased enzymatic activity for cleaving and releasing the tumour
CC necrosis factor (TNF) receptor in genetically modified COS-1 cells
CC expressing the receptor. Methods from the present invention can be used
CC to assess a disease condition associated with altered TRRE activity. The
CC polypeptides, polynucleotides and antibodies can be used to decrease or
CC increase signal transduction from a cytokine in a cell. The polypeptides,
CC polynucleotides and antibodies may be used to treat heart failure,
CC cachexia, inflammation, endotoxin shock, arthritis, multiple sclerosis
CC and sepsis, and cancer. The present sequence represents the longest open
CC reading frame encoded by the complementary strand of the AIM2 clone which
CC affects tumour necrosis factor receptor releasing enzyme (TRRE) activity
XX
SQ Sequence 474 AA;
Query Match 90.3%; Score 28; DB 3; Length 474;
Best Local Similarity 85.7%; Pred. No. 8.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LTLKLSR 7
Db 358 LTLRLSR 364

```
RESULT 13
ADJ49412
ID ADJ49412 standard; protein; 633 AA.
XX
AC ADJ49412;
XX
DT 06-MAY-2004 (first entry)
XX
DE Oil-associated gene related protein #912.
XX
KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
XX
OS Unidentified.
XX
PN US2004025202-A1.
XX
PD 05-FEB-2004.
XX
PF 14-MAR-2003; 2003US-00389566.
XX
PR 15-MAR-2002; 2002US-0365301P.
XX
PR 26-JUN-2002; 2002US-0391786P.
XX
PR 26-JUN-2002; 2002US-0392018P.
XX
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
XX
PI Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
XX
DR WPI; 2004-142683/14.
XX
PT Novel recombinant DNA construct comprising a promoter functional in
PT plants operably linked to an oil-associated gene for producing transgenic
PT plant seed.
XX
PS Example 3; SEQ ID NO 1416; 22pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in plants operably linked to an oil-associated gene.
CC The construct is useful for transgenic plant seed which has in its genome
CC the construct, that is functional in the plant to transcribe the oil-
CC associated gene. The transgenic plant seed grows into a plant having
CC enhanced seed oil as compared to wild type. The construct is useful for
CC producing hybrid maize seed. The transgenic plant seed is useful for
CC producing vegetable oil. The present sequence represents the amino acid
CC sequence of an oil-associated gene related protein.
XX
SQ Sequence 633 AA;

Query Match 90.3%; Score 28; DB 8; Length 633;
Best Local Similarity 85.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
Db 291 LTLKLTR 297

RESULT 14
ADJ49826
ID ADJ49826 standard; protein; 638 AA.
XX
AC ADJ49826;
XX
DT 06-MAY-2004 (first entry)
XX
DE Oil-associated gene related protein #1326.
XX
KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
XX
```

```
OS Unidentified.
XX
PN US2004025202-A1.
XX
PD 05-FEB-2004.
XX
PF 14-MAR-2003; 2003US-00389566.
XX
PR 15-MAR-2002; 2002US-0365301P.
XX
PR 26-JUN-2002; 2002US-0391786P.
XX
PR 26-JUN-2002; 2002US-0392018P.
XX
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
XX
PI Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
XX
DR WPI; 2004-142683/14.
XX
PT Novel recombinant DNA construct comprising a promoter functional in
PT plants operably linked to an oil-associated gene for producing transgenic
PT plant seed.
XX
PS Example 3; SEQ ID NO 1830; 22pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in plants operably linked to an oil-associated gene.
CC The construct is useful for transgenic plant seed which has in its genome
CC the construct, that is functional in the plant to transcribe the oil-
CC associated gene. The transgenic plant seed grows into a plant having
CC enhanced seed oil as compared to wild type. The construct is useful for
CC producing hybrid maize seed. The transgenic plant seed is useful for
CC producing vegetable oil. The present sequence represents the amino acid
CC sequence of an oil-associated gene related protein.
XX
SQ Sequence 638 AA;

Query Match 90.3%; Score 28; DB 8; Length 638;
Best Local Similarity 85.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
Db 291 LTLKLTR 297

RESULT 15
ADJ49161
ID ADJ49161 standard; protein; 638 AA.
XX
AC ADJ49161;
XX
DT 06-MAY-2004 (first entry)
XX
DE Oil-associated gene related protein #661.
XX
KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
XX
OS Unidentified.
XX
PN US2004025202-A1.
XX
PD 05-FEB-2004.
XX
PF 14-MAR-2003; 2003US-00389566.
XX
PR 15-MAR-2002; 2002US-0365301P.
XX
PR 26-JUN-2002; 2002US-0391786P.
XX
PR 26-JUN-2002; 2002US-0392018P.
XX
```

PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
XX
PI Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
XX
DR WPI; 2004-142683/14.
XX
PT Novel recombinant DNA construct comprising a promoter functional in
PT plants operably linked to an oil-associated gene for producing transgenic
PT plant seed.
XX
PS Example 3; SEQ ID NO 1165; 22pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in plants operably linked to an oil-associated gene.
CC The construct is useful for transgenic plant seed which has in its genome
CC the construct, that is functional in the plant to transcribe the oil-
CC associated gene. The transgenic plant seed grows into a plant having
CC enhanced seed oil as compared to wild type. The construct is useful for
CC producing hybrid maize seed. The transgenic plant seed is useful for
CC producing vegetable oil. The present sequence represents the amino acid
CC sequence of an oil-associated gene related protein.
XX
SQ Sequence 638 AA;

Query Match 90.3%; Score 28; DB 8; Length 638;
Best Local Similarity 85.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
|||:|
Db 291 LTLKLTR 297

Search completed: November 4, 2004, 00:47:44
Job time : 63.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:48:50 ; Search time 72.3333 Seconds
(without alignments)
31.376 Million cell updates/sec

Title: US-09-712-819D-13
Perfect score: 31
Sequence: 1 LTLKLSR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0
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Listing first 45 summaries

Database : Published Applications AA:*

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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	31	100.0	382	14	US-10-369-493-5663	Sequence 5663, Ap
2	29	93.5	638	15	US-10-389-566-1774	Sequence 1774, Ap
3	29	93.5	641	15	US-10-389-566-1393	Sequence 1393, Ap
4	29	93.5	641	15	US-10-389-566-2249	Sequence 2249, Ap
5	29	93.5	726	14	US-10-369-493-5945	Sequence 5945, Ap
6	28	90.3	474	9	US-09-752-639-148	Sequence 148, App
7	28	90.3	474	9	US-09-984-198-148	Sequence 148, App
8	28	90.3	629	14	US-10-369-493-11797	Sequence 11797, A
9	28	90.3	630	14	US-10-369-493-14521	Sequence 14521, A
10	28	90.3	633	14	US-10-369-493-14213	Sequence 14213, A
11	28	90.3	633	14	US-10-369-493-14987	Sequence 14987, A
12	28	90.3	633	15	US-10-389-566-1416	Sequence 1416, Ap
13	28	90.3	638	14	US-10-369-493-12088	Sequence 12088, A

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14 28 90.3 638 15 US-10-389-566-1165 Sequence 1165, Ap
15 28 90.3 638 15 US-10-389-566-1830 Sequence 1830, Ap
16 28 90.3 1522 14 US-10-134-102-8 Sequence 8, Appli
17 28 90.3 1522 14 US-10-144-198-31 Sequence 31, Appl
18 28 90.3 2697 14 US-10-144-198-12 Sequence 12, Appl
19 27 87.1 31 14 US-10-001-883-131 Sequence 131, App
20 27 87.1 66 15 US-10-424-599-190772 Sequence 190772,
21 27 87.1 123 15 US-10-424-599-281882 Sequence 281882,
22 27 87.1 127 9 US-09-753-436-45 Sequence 45, Appl
23 27 87.1 127 14 US-10-163-942-45 Sequence 45, Appl
24 27 87.1 132 15 US-10-424-599-161373 Sequence 161373,
25 27 87.1 133 14 US-10-153-382-39 Sequence 39, Appl
26 27 87.1 189 9 US-09-815-242-11799 Sequence 11799, A
27 27 87.1 189 15 US-10-282-122A-66201 Sequence 66201, A
28 27 87.1 189 15 US-10-424-599-158936 Sequence 158936,
29 27 87.1 191 15 US-10-282-122A-63672 Sequence 63672, A
30 27 87.1 259 15 US-10-289-762-366 Sequence 366, App
31 27 87.1 259 15 US-10-282-122A-54805 Sequence 54805, A
32 27 87.1 259 15 US-10-282-122A-55147 Sequence 55147, A
33 27 87.1 291 15 US-10-424-599-209007 Sequence 209007,
34 27 87.1 626 15 US-10-380-533-144 Sequence 144, App
35 27 87.1 645 15 US-10-389-566-1037 Sequence 1037, Ap
36 27 87.1 706 15 US-10-380-533-134 Sequence 134, App
37 27 87.1 707 15 US-10-380-533-142 Sequence 142, App
38 26 83.9 35 15 US-10-424-599-163720 Sequence 163720,
39 26 83.9 42 15 US-10-424-599-159705 Sequence 159705,
40 26 83.9 57 15 US-10-424-599-277603 Sequence 277603,
41 26 83.9 60 9 US-09-864-761-43672 Sequence 43672, A
42 26 83.9 66 9 US-09-867-550-1190 Sequence 1190, Ap
43 26 83.9 74 15 US-10-424-599-176978 Sequence 176978,
44 26 83.9 77 15 US-10-424-599-279709 Sequence 279709,
45 26 83.9 78 15 US-10-424-599-191620 Sequence 191620,

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ALIGNMENTS

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RESULT 1
US-10-369-493-5663
; Sequence 5663, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5663
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5663

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Query Match 100.0%; Score 31; DB 14; Length 382;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 LTLKLSR 7
Db 73 LTLKLSR 79

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RESULT 2
US-10-389-566-1774
; Sequence 1774, Application US/10389566

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; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1774
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Geobacter metallireducens
US-10-389-566-1774

Query Match          93.5%; Score 29; DB 15; Length 638;
Best Local Similarity 85.7%; Pred. No. 6.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LTLKLSR 7
Db      291 LTMKLSR 297

RESULT 3
US-10-389-566-1393
; Sequence 1393, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1393
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Sinorhizobium meliloti
US-10-389-566-1393

Query Match          93.5%; Score 29; DB 15; Length 641;
Best Local Similarity 85.7%; Pred. No. 6.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LTLKLSR 7
Db      291 LTMKLSR 297

RESULT 4
US-10-389-566-2249
; Sequence 2249, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants

```

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; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2249
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Sinorhizobium meliloti
US-10-389-566-2249

Query Match          93.5%; Score 29; DB 15; Length 641;
Best Local Similarity 85.7%; Pred. No. 6.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LTLKLSR 7
Db      291 LTMKLSR 297

RESULT 5
US-10-369-493-5945
; Sequence 5945, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5945
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5945

Query Match          93.5%; Score 29; DB 14; Length 726;
Best Local Similarity 85.7%; Pred. No. 7.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LTLKLSR 7
Db      512 LTLKISR 518

RESULT 6
US-09-752-639-148
; Sequence 148, Application US/09752639
; Patent No. US20020091243A1
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, T.
; APPLICANT: Granger, G.A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
; TITLE OF INVENTION: of Use Thereof
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD

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/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304-1018
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: Windows
/ SOFTWARE: FastSEQ for Windows Version 2.0b
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/752,639
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA: PCT/US99/10793
/ APPLICATION NUMBER: 09/081,385
/ FILING DATE:
/ APPLICATION NUMBER: 08/964,747
/ FILING DATE: 05-NOV-1997
/ APPLICATION NUMBER: 60/030,761
/ FILING DATE: 06-NOV-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Wu, Frank
/ REGISTRATION NUMBER: 41,386
/ REFERENCE/DOCKET NUMBER: 22000-20577.21
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-813-5600
/ TELEFAX: 650-494-0792
/ TELEX: 706141
/ INFORMATION FOR SEQ ID NO: 148:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 474 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/ US-09-752-639-148

Query Match 90.3%; Score 28; DB 9; Length 474;
Best Local Similarity 85.7%; Pred. No. 7.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
|||:|
Db 358 LTLRLSR 364

RESULT 7
US-09-984-198-148
/ Sequence 148, Application US/09984198
/ Patent No. US20020106679A1
/ GENERAL INFORMATION:
/ APPLICANT: Gatanaga, T.
/ APPLICANT: Granger, G.A.
/ TITLE OF INVENTION: Factors Altering Tumor Necrosis
/ TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
/ TITLE OF INVENTION: of Use Thereof
/ NUMBER OF SEQUENCES: 154
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: MORRISON & FOERSTER
/ STREET: 755 PAGE MILL ROAD
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304-1018
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: Windows
/ SOFTWARE: FastSEQ for Windows Version 2.0b
/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/984,198
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA: PCT/US99/10793
/ APPLICATION NUMBER: 09/081,385
/ FILING DATE:
/ APPLICATION NUMBER: 08/964,747
/ FILING DATE: 05-NOV-1997
/ APPLICATION NUMBER: 60/030,761
/ FILING DATE: 06-NOV-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Wu, Frank
/ REGISTRATION NUMBER: 41,386
/ REFERENCE/DOCKET NUMBER: 22000-20577.21
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-813-5600
/ TELEFAX: 650-494-0792
/ TELEX: 706141
/ INFORMATION FOR SEQ ID NO: 148:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 474 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/ US-09-984-198-148

Query Match 90.3%; Score 28; DB 9; Length 474;
Best Local Similarity 85.7%; Pred. No. 7.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
|||:|
Db 358 LTLRLSR 364

RESULT 8
US-10-369-493-11797
/ Sequence 11797, Application US/10369493
/ Publication No. US20030233675A1
/ GENERAL INFORMATION:
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Hinkle, Gregory J.
/ APPLICANT: Slater, Steven C.
/ APPLICANT: Goldman, Barry S.
/ APPLICANT: Chen, Xianfeng
/ TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
/ TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
/ FILE REFERENCE: 38-10(52052)B
/ CURRENT APPLICATION NUMBER: US/10/369,493
/ CURRENT FILING DATE: 2003-02-28
/ PRIOR APPLICATION NUMBER: US 60/360,039
/ PRIOR FILING DATE: 2002-02-21
/ NUMBER OF SEQ ID NOS: 47374
/ SEQ ID NO 11797
/ LENGTH: 629
/ TYPE: PRT
/ ORGANISM: Agrobacterium tumefaciens
/ US-10-369-493-11797

Query Match 90.3%; Score 28; DB 14; Length 629;
Best Local Similarity 85.7%; Pred. No. 1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
|||:|
Db 291 LTLKLTR 297

RESULT 9


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US-10-369-493-14521
; Sequence 14521, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14521
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14521

Query Match          90.3%; Score 28; DB 14; Length 630;
Best Local Similarity 85.7%; Pred. No. 1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LTLKLSR 7
      |||||:|
Db      291 LTLKLTR 297

RESULT 10
US-10-369-493-14213
; Sequence 14213, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14213
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14213

Query Match          90.3%; Score 28; DB 14; Length 633;
Best Local Similarity 85.7%; Pred. No. 1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LTLKLSR 7
      |||||:|
Db      291 LTLKLTR 297

RESULT 11
US-10-369-493-14987
; Sequence 14987, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
```

```
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14987
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14987

Query Match          90.3%; Score 28; DB 14; Length 633;
Best Local Similarity 85.7%; Pred. No. 1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LTLKLSR 7
      |||||:|
Db      291 LTLKLTR 297

RESULT 12
US-10-389-566-1416
; Sequence 1416, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1416
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-389-566-1416

Query Match          90.3%; Score 28; DB 15; Length 633;
Best Local Similarity 85.7%; Pred. No. 1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LTLKLSR 7
      |||||:|
Db      291 LTLKLTR 297

RESULT 13
US-10-369-493-12088
; Sequence 12088, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
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; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 12088
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Mesorhizobium loti
US-10-369-493-12088
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Query Match          90.3%; Score 28; DB 14; Length 638;
Best Local Similarity 85.7%; Pred. No. 1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LTLKLSR 7
        |||||:|
Db      291 LTLKLTR 297
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RESULT 14

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US-10-389-566-1165
; Sequence 1165, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1165
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Mesorhizobium loti
US-10-389-566-1165
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Query Match          90.3%; Score 28; DB 15; Length 638;
Best Local Similarity 85.7%; Pred. No. 1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LTLKLSR 7
        |||||:|
Db      291 LTLKLTR 297
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RESULT 15

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US-10-389-566-1830
; Sequence 1830, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1830
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; LENGTH: 638
; TYPE: PRT
; ORGANISM: Rhizobium leguminosarum
US-10-389-566-1830
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Query Match          90.3%; Score 28; DB 15; Length 638;
Best Local Similarity 85.7%; Pred. No. 1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LTLKLSR 7
        |||||:|
Db      291 LTLKLTR 297
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OM protein - protein search, using sw model

Run on: November 4, 2004, 01:09:51 ; Search time 23.6667 Seconds
(without alignments)
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Title: US-09-712-819D-12
Perfect score: 33
Sequence: 1 FTLEISR 7

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Searched: 478139 seqs, 66318000 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	24	72.7	7	1	US-08-222-619-8
2	24	72.7	7	5	PCT-US95-04075-8
3	20	60.6	7	4	US-09-423-468A-6
4	19	57.6	6	1	US-08-222-619-21
5	19	57.6	6	5	PCT-US95-04075-21
6	19	57.6	7	1	US-08-136-743B-55
7	19	57.6	7	3	US-09-040-216-28
8	18	54.5	6	1	US-08-297-731-4
9	18	54.5	6	3	US-09-623-618B-6
10	18	54.5	6	4	US-09-657-332A-6
11	18	54.5	6	4	US-09-876-388-6
12	18	54.5	6	5	PCT-US95-10793-4
13	18	54.5	7	1	US-08-297-731-5
14	18	54.5	7	3	US-09-623-618B-7
15	18	54.5	7	3	US-09-218-363-23
16	18	54.5	7	4	US-09-657-332A-7
17	18	54.5	7	4	US-09-876-388-7
18	18	54.5	7	4	US-08-753-750B-20
19	18	54.5	7	5	PCT-US95-10793-5
20	17	51.5	5	1	US-08-136-743B-63
21	17	51.5	5	3	US-09-040-216-55
22	17	51.5	5	3	US-08-591-632-23
23	17	51.5	5	3	US-09-611-451-23
24	17	51.5	6	1	US-08-136-743B-62
25	17	51.5	6	3	US-09-040-216-54
26	17	51.5	6	3	US-09-187-859-636
27	17	51.5	6	3	US-09-187-859-650

28	17	51.5	6	4	US-09-522-433B-12	Sequence 12, Appl
29	17	51.5	6	4	US-09-839-542B-636	Sequence 636, App
30	17	51.5	6	4	US-09-839-542B-650	Sequence 650, App
31	17	51.5	7	1	US-09-393-941-2	Sequence 2, Appli
32	17	51.5	7	1	US-08-136-743B-6	Sequence 6, Appli
33	17	51.5	7	1	US-08-136-743B-29	Sequence 29, Appl
34	17	51.5	7	1	US-08-136-743B-33	Sequence 33, Appl
35	17	51.5	7	1	US-08-136-743B-37	Sequence 37, Appl
36	17	51.5	7	1	US-08-136-743B-54	Sequence 54, Appl
37	17	51.5	7	1	US-08-136-743B-56	Sequence 56, Appl
38	17	51.5	7	1	US-08-136-743B-57	Sequence 57, Appl
39	17	51.5	7	1	US-08-136-743B-58	Sequence 58, Appl
40	17	51.5	7	1	US-08-136-743B-59	Sequence 59, Appl
41	17	51.5	7	1	US-08-136-743B-60	Sequence 60, Appl
42	17	51.5	7	1	US-08-175-471-2	Sequence 2, Appli
43	17	51.5	7	2	US-08-429-054A-2	Sequence 2, Appli
44	17	51.5	7	2	US-08-718-777-2	Sequence 2, Appli
45	17	51.5	7	3	US-09-040-216-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-222-619-8
; Sequence 8, Application US/08222619
; Patent No. 5652352
; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henri
; APPLICANT: Lyons, David
; APPLICANT: Wurfel, Mark
; APPLICANT: Wright, Samuel
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Center, Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,619
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-222-619-8

Query Match 72.7%; Score 24; DB 1; Length 7;
Best Local Similarity 71.4%; Pred. No. 3.8e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTLEISR 7
|||
Db 1 FTTFYSR 7

RESULT 2
PCT-US95-04075-8
; Sequence 8, Application PC/TUS9504075
; GENERAL INFORMATION:

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; APPLICANT: AMGEN INC.
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Center, Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04075
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; PCT-US95-04075-8

Query Match 72.7%; Score 24; DB 5; Length 7;
Best Local Similarity 71.4%; Pred. No. 3.8e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FTLEISR 7
Db 1 FTFEYSR 7

RESULT 3
US-09-423-468A-6
; Sequence 6, Application US/09423468A
; Patent No. 6469149
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnol
; APPLICANT: Guy Jerome Corneel Bauw
; APPLICANT: Mark William Davey
; APPLICANT: Jens Ostergaard
; APPLICANT: Marc Charles Ernest Van Montagu
; TITLE OF INVENTION: PRODUCTION OF ASCORBIC ACID IN PLANTS
; FILE REFERENCE: DECLES.001APC
; CURRENT APPLICATION NUMBER: US/09/423,468A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: NL 1006000
; PRIOR FILING DATE: 1997-05-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Brassica oleracea
; US-09-423-468A-6

Query Match 60.6%; Score 20; DB 4; Length 7;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLEISR 7
Db 2 TLELSK 7

RESULT 4
US-08-222-619-21

Query Match 57.6%; Score 19; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FTLEIS 6
Db 1 FTFEYS 6

RESULT 5
PCT-US95-04075-21
; Sequence 21, Application PC/TUS9504075
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Center, Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04075
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-222-619-21

; Sequence 21, Application US/08222619
; Patent No. 5652352
; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henri
; APPLICANT: Lyons, David
; APPLICANT: Wurfel, Mark
; APPLICANT: Wright, Samuel
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Center, Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,619
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-222-619-21
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/
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
PCT-US95-04075-21

Query Match          57.6%; Score 19; DB 5; Length 6;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTLEIS 6
   |||||
Db 1 FTFEYS 6

RESULT 6
US-08-136-743B-55
; Sequence 55, Application US/08136743B
; Patent No. 5459063
; GENERAL INFORMATION:
; APPLICANT: Barry S. Cooperman, Harvey Rubin,
; APPLICANT: Jerome Salem, and Alison L. Fisher
; TITLE OF INVENTION: "Plasmodium falciparum Ribonu-
; TITLE OF INVENTION: cleotide Reductase, DNA Sequences Therefor and Peptide inhibit
; TITLE OF INVENTION: Thereof"
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The University of Pennsylvania
; STREET: Suite 330
; STREET: 3700 Market Street
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19104-3246
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/136,743B
; FILING DATE: 10/14/93
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 3957-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5459063e
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-136-743B-55

Query Match          57.6%; Score 19; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEI 5
   |||||
Db 1 FTLDL 5

RESULT 7
US-09-040-216-28
; Sequence 28, Application US/09040216
; Patent No. 6030942
; GENERAL INFORMATION:
; APPLICANT: COOPERMAN, ET AL., BARRY
; TITLE OF INVENTION: PEPTIDES, PEPTIDE ANALOGS, PEPTIDOMIMETICS, AND OTHER
; TITLE OF INVENTION: SMALL MOLECULES USEFUL FOR INHIBITING THE ACTIVITY OF
```

```
/
/ TITLE OF INVENTION: RIBONUCLEOTIDE REDUCTASE
/ FILE REFERENCE: 9596-63UI
/ CURRENT APPLICATION NUMBER: US/09/040,216
/ CURRENT FILING DATE: 1998-03-17
/ EARLIER APPLICATION NUMBER: 08/919,748
/ EARLIER FILING DATE: 1997-08-28
/ EARLIER APPLICATION NUMBER: 60/025,146
/ EARLIER FILING DATE: 1996-08-30
/ NUMBER OF SEQ ID NOS: 61
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 28
/ LENGTH: 7
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: Ribonucleotide reductase inhibitor peptide
/ FEATURE:
/ OTHER INFORMATION: residue 1: MOD_RES: ACETYLATION
US-09-040-216-28

Query Match          57.6%; Score 19; DB 3; Length 7;
Best Local Similarity 60.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEI 5
   |||||
Db 1 FTLDL 5

RESULT 8
US-08-297-731-4
; Sequence 4, Application US/08297731
; Patent No. 5574008
; GENERAL INFORMATION:
; APPLICANT: Johnson, William T.
; APPLICANT: Yakubu-Madus, Fatima E.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE FRAGMENTS OF
; TITLE OF INVENTION: GLUCAGON-LIKE INSULINOTROPIC PEPTIDE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company/RSM
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/297,731
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Maciak, Ronald S.
; REGISTRATION NUMBER: 35,262
; REFERENCE/DOCKET NUMBER: X9630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-1664
; TELEFAX: 317-277-1917
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-297-731-4

Query Match          54.5%; Score 18; DB 1; Length 6;
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Best Local Similarity 50.0%; Pred. No. 3.8e+05; Indels 0; Gaps 0;
Matches 3; Conservative 2; Mismatches 1;

QY 1 FTLEIS 6
|| :|
Db 1 FTSDVS 6

RESULT 9

US-09-623-618B-6
; Sequence 6, Application US/09623618B
; Patent No. 6329336
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: L'Archeveque, Benoit
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Leblanc, Anouk
; APPLICANT: St. Pierre, Serge
; TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES
; FILE REFERENCE: 500862001620
; CURRENT APPLICATION NUMBER: US/09/623,618B
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: PCT/US00/13563
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-618B-6

Query Match 54.5%; Score 18; DB 3; Length 6;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEIS 6
|| :|
Db 1 FTSDVS 6

RESULT 10

US-09-657-332A-6
; Sequence 6, Application US/09657332A
; Patent No. 6514500
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: L'Archeveque, Benoit
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Leblanc, Anouk
; APPLICANT: St. Pierre, Serge
; TITLE OF INVENTION: LONG LASTING SYNTHETIC GLUCAGON LIKE PEPTIDE (GLP-1)
; FILE REFERENCE: 500862001600
; CURRENT APPLICATION NUMBER: US/09/657,332A
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-332A-6

Query Match 54.5%; Score 18; DB 4; Length 6;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEIS 6
|| :|
Db 1 FTSDVS 6

RESULT 11

US-09-876-388-6
; Sequence 6, Application US/09876388
; Patent No. 6593295
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: L'Archeveque, Benoit
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Leblanc, Anouk
; APPLICANT: St. Pierre, Serge
; TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES
; FILE REFERENCE: 500862001610
; CURRENT APPLICATION NUMBER: US/09/876,388
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/623,618
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: PCT/US00/13563
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-876-388-6

Query Match 54.5%; Score 18; DB 4; Length 6;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEIS 6
|| :|
Db 1 FTSDVS 6

RESULT 12

PCT-US95-10793-4
; Sequence 4, Application PC/TUS9510793
; GENERAL INFORMATION:
; APPLICANT: Johnson, William T.
; APPLICANT: Yakubu-Madus, Fatima E.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE FRAGMENTS OF
; TITLE OF INVENTION: GLUCAGON-LIKE INSULINOTROPIC PEPTIDE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company/RSM
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: IN
; COUNTRY: USA

```
;
;
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10793
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maciak, Ronald S.
; REGISTRATION NUMBER: 35,262
; REFERENCE/DOCKET NUMBER: X9630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-1664
; TELEFAX: 317-277-1917
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US95-10793-4

Query Match          54.5%; Score 18; DB 5; Length 6;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FTLEIS 6
Db      1 FTSDVS 6

RESULT 13
US-08-297-731-5
; Sequence 5, Application US/08297731
; Patent No. 5574008
; GENERAL INFORMATION:
; APPLICANT: Johnson, William T.
; APPLICANT: Yakubu-Madus, Fatima E.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE FRAGMENTS OF
; TITLE OF INVENTION: GLUCAGON-LIKE INSULINOTROPIC PEPTIDE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company/RSM
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/297,731
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Maciak, Ronald S.
; REGISTRATION NUMBER: 35,262
; REFERENCE/DOCKET NUMBER: X9630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-1664
; TELEFAX: 317-277-1917
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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;
;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-297-731-5

Query Match          54.5%; Score 18; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FTLEIS 6
Db      2 FTSDVS 7

RESULT 14
US-09-623-618B-7
; Sequence 7, Application US/09623618B
; Patent No. 6329336
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: L'Archeveque, Benoit
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Leblanc, Anouk
; APPLICANT: St. Pierre, Serge
; TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES
; FILE REFERENCE: 500862001620
; CURRENT APPLICATION NUMBER: US/09/623,618B
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: PCT/US00/13563
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
; US-09-623-618B-7

Query Match          54.5%; Score 18; DB 3; Length 7;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FTLEIS 6
Db      2 FTSDVS 7

RESULT 15
US-09-218-363-23
; Sequence 23, Application US/09218363
; Patent No. 6387616
; GENERAL INFORMATION:
; APPLICANT: Ozellus, Laurie J.
; APPLICANT: Breakfield, Xandra O.
; TITLE OF INVENTION: TORSIN, TORSIN GENES, AND METHODS OF USE
; FILE REFERENCE: MGH-1184pA2
; CURRENT APPLICATION NUMBER: US/09/218,363
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 09/099,454
; EARLIER FILING DATE: 1998-06-18
; EARLIER APPLICATION NUMBER: 60/050,244
; EARLIER FILING DATE: 1997-06-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 7
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us-09-712-819d-12.closed.ra

Thu Nov 4 07:26:49 2004

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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-218-363-23

Query Match      54.5%; Score 18; DB 3; Length 7;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FTLE 4
      |||
Db      2 FTME 5

Search completed: November 4, 2004, 01:25:35
Job time : 24.6667 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 01:09:31 ; Search time 18.3333 Seconds
(without alignments)
36.737 Million cell updates/sec

Title: US-09-712-819D-12
Perfect score: 33
Sequence: 1 FTLEISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	13	39.4	6	2 B26206	alpha-1,4-glucan-p
2	13	39.4	7	2 E48394	glycoprotein compo
3	13	39.4	7	2 I48086	DNA topoisomerase
4	13	39.4	7	2 B48394	major fat-globule
5	12	36.4	5	2 T14910	hypothetical prote
6	11	33.3	4	2 A61300	22K superhelical D
7	11	33.3	5	2 PT0644	T-cell receptor be
8	11	33.3	7	2 S19630	ribosomal protein
9	10	30.3	5	2 A60521	glycogen phosphory
10	10	30.3	7	2 B39127	phosphotransferase
11	10	30.3	7	2 PS0254	18K protein 5507 -
12	10	30.3	7	2 S33244	neuromodulatory pe
13	10	30.3	7	2 S33245	neuromodulatory pe
14	9	27.3	3	3 T13892	cytochrome-c oxida
15	9	27.3	5	2 A44955	alkalai monooxygen
16	9	27.3	5	2 S11127	phosphoprotein, bo
17	9	27.3	5	2 PT0525	T-cell receptor be
18	9	27.3	5	2 PT0577	T-cell receptor be
19	9	27.3	5	2 PT0700	T-cell receptor be
20	9	27.3	5	2 S69237	surface protein te
21	9	27.3	5	2 E42364	flagellar protein
22	9	27.3	5	2 PT0565	T-cell receptor be
23	9	27.3	5	2 B34835	dnaA protein - pse
24	9	27.3	6	2 A60986	N-formyl oligopept
25	9	27.3	6	2 T11779	phosphoglycerate t
26	9	27.3	6	2 A43766	28K ubiquitin-immu
27	9	27.3	6	2 JH0784	neuropeptide TE-6
28	9	27.3	6	2 I37263	protein - human
29	9	27.3	6	2 S78764	ribosomal protein

30	9	27.3	6	2 A20186	fatty-acid synthas
31	9	27.3	6	2 I65546	MHC H2-L antigen -
32	9	27.3	6	2 PT0518	T-cell receptor be
33	9	27.3	6	2 PT0662	T-cell receptor be
34	9	27.3	7	2 JN0859	peptidyl-dipeptida
35	9	27.3	7	2 S25266	p1E protein - Esc
36	9	27.3	7	2 A28709	phosphonoacetaldeh
37	9	27.3	7	2 PN0150	omega-gliadine 1'
38	9	27.3	7	2 PT0269	Ig heavy chain CRD
39	9	27.3	7	2 E30608	Ig kappa chain V-I
40	9	27.3	7	2 PT0671	T-cell receptor be
41	9	27.3	7	2 A38671	peptidylglycine mo
42	9	27.3	7	2 A58718	carnocin UI49 - Ca
43	9	27.3	7	2 S45648	Na+-transporting A
44	9	27.3	7	2 PN0649	pullulanase (EC 3.
45	9	27.3	7	2 A15398	choline oxidase (E

ALIGNMENTS

RESULT 1
B26206

alpha-1,4-glucan-protein synthase (UDP-forming) (EC 2.4.1.112) - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 13-Sep-1996
C;Accession: B26206; A26206

R;Larner, J.; Sanger, F.

J. Mol. Biol. 11, 491-500, 1965

A;Title: The amino acid sequence of the phosphorylation site of muscle uridine diphosphat

A;Reference number: A26206

A;Accession: B26206

A;Molecule type: protein

A;Residues: 1-6 <LAR>

A;Experimental source: muscle

A;Note: Lys-1 was also found

C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein

F;4/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 39.4%; Score 13; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIS 6
|||
Db 2 EIS 4

RESULT 2
E48394

glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr

C;Species: Bos primigenius taurus (cattle)

C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997

C;Accession: E48394

R;Mather, I.H.; Banghart, L.R.; Lane, W.S.

Biochem. Mol. Biol. Int. 29, 545-554, 1993

A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig

II-like sequences.

A;Reference number: A48394; MUID:93250576; PMID:8485470

A;Accession: E48394

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <MAT>

A;Experimental source: milk

A;Note: sequence extracted from NCBI backbone (NCBIP:131450)

C;Keywords: glycoprotein

Query Match

Best Local Similarity 39.4%; Score 13; DB 2; Length 7;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 EISR 7
|::|

Db	4	ELAR 7	Best Local Similarity 66.7%; Pred. No. 2.8e+05; Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
RESULT 3			
I48086			
DNA topoisomerase II alpha - Chinese hamster (fragment)			
C;Species: Cricetulus griseus (Chinese hamster)			
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999			
C;Accession: I48086			
R;Ng, S.W.; Eder, J.P.; Schnipper, L.E.; Chan, V.T.W.			
J. Biol. Chem. 270, 25850-25858, 1995			
A;Title: Molecular cloning and characterization of the promoter for the Chinese hamster			
A;Reference number: I48086; MUID:96029684; PMID:7592770			
A;Accession: I48086			
A;Status: preliminary; translated from GB/EMBL/DBJ			
A;Molecule type: DNA			
A;Residues: 1-7 <RBS>			
A;Cross-references: EMBL:U34196; NID:g1041231; PIDN:AAC52315.1; PID:g1041232			
Query Match 39.4%; Score 13; DB 2; Length 7;			
Best Local Similarity 50.0%; Pred. No. 2.8e+05;			
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;			
QY	3	LEIS 6	
: :			
Db	1	MELS 4	
RESULT 4			
B48394			
major fat-globule membrane protein GP 55 - guinea pig (fragment)			
C;Species: Cavia porcellus (guinea pig)			
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995			
C;Accession: B48394			
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.			
Biochem. Mol. Biol. Int. 29, 545-554, 1993			
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig			
II-like sequences.			
A;Reference number: A48394; MUID:93250576; PMID:8485470			
A;Accession: B48394			
A;Status: preliminary			
A;Molecule type: protein			
A;Residues: 1-7 <MAT>			
A;Experimental source: milk			
A;Note: sequence extracted from NCBI backbone (NCBIP:131444)			
Query Match 39.4%; Score 13; DB 2; Length 7;			
Best Local Similarity 50.0%; Pred. No. 2.8e+05;			
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;			
QY	4	EISR 7	
: :			
Db	4	ELAR 7	
RESULT 5			
T14910			
hypothetical protein - parsley			
C;Species: Petroselinum crispum (parsley)			
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000			
C;Accession: T14910			
R;Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.			
Mol. Gen. Genet. 257, 595-605, 1998			
A;Title: CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis of			
A;Reference number: Z18261; MUID:98285918; PMID:9604882			
A;Accession: T14910			
A;Status: preliminary; translated from GB/EMBL/DBJ			
A;Molecule type: mRNA			
A;Residues: 1-5 <KIR>			
A;Cross-references: EMBL:Y10810; NID:g3336904; PIDN:CAA71769.1; PID:g3336905			
A;Experimental source: ssp. Hamburger Schnitt			
Query Match 36.4%; Score 12; DB 2; Length 5;			
Best Local Similarity 100.0%; Pred. No. 2.8e+05;			
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	FT 2	
:			
Db	4	FT 5	
RESULT 8			
S19630			
ribosomal protein L30 - Streptomyces griseus (fragment)			
C;Species: Streptomyces griseus			
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 06-Jun-1997			
C;Accession: S19630			
R;Ochi, K.			
Int. J. Syst. Bacteriol. 42, 144-150, 1992			
A;Title: Electrophoretic heterogeneity of ribosomal protein AT-L30 among actinomycete			
A;Reference number: S19630; MUID:92144363; PMID:1736962			
A;Accession: S19630			
A;Molecule type: protein			
A;Residues: 1-7 <OCH>			

A;Experimental source: strain IFO 13189
C;Superfamily: Escherichia coli ribosomal protein L30
C;Keywords: protein biosynthesis; ribosome

Query Match 33.3%; Score 11; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 LEISR 7

Db 3 LKITQ 7

RESULT 9

A60521

glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)

N;Alternate names: glycogen phosphorylase b

C;Species: Liza ramada

C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Mar-2004

C;Accession: A60521

R;Bonamusa, L.; Baanante, I.V.

Comp. Biochem. Physiol. B 95, 295-301, 1990

A;Title: Purification and characterization of glycogen phosphorylase B from skeletal muscle

A;Reference number: A60521; PMID:90227907; PMID:2109669

A;Accession: A60521

A;Molecule type: protein

A;Residues: 1-5 <BON>

C;Keywords: Glycosyltransferase; hexosyltransferase; phosphoprotein

F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experiment

Query Match

Best Local Similarity 30.3%; Score 10; DB 2; Length 5;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIS 6

Db 1 QIS 3

RESULT 10

B39127

phosphotransferase system enzyme II (EC 2.7.1.69) - Escherichia coli (fragment)

C;Species: Escherichia coli

C;Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 08-Oct-1999

C;Accession: B39127

R;Hardesty, C.; Ferran, C.; Di Rienzo, J.M.

J. Bacteriol. 173, 449-456, 1991

A;Title: Plasmid-mediated sucrose metabolism in Escherichia coli: characterization of sucrose

A;Reference number: A39127; PMID:91100329; PMID:1846143

A;Accession: B39127

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-7 <HAR>

A;Cross-references: GB:M38416; NID:G155142; PIDN:AAA98418.1; PID:G155144

C;Keywords: phosphotransferase

Query Match

Best Local Similarity 30.3%; Score 10; DB 2; Length 7;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIS 6

Db 5 QIS 7

RESULT 11

PS0254

18K protein 5507 - rice (strain Nihonbare) (fragment)

C;Species: Oryza sativa (rice)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Mar-1995

C;Accession: PS0254

R;Tsugita, A.

submitted to JIPID, April 1993

A;Reference number: PS0206

A;Accession: PS0254

A;Molecule type: protein

A;Residues: 1-7 <TSU>

A;Experimental source: leaf, chloroplast, strain Nihonbare

A;Note: molecular weight 18K, pI 4.4

Query Match

Best Local Similarity 30.3%; Score 10; DB 2; Length 7;

Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 LEISR 7

Db 1 LAIAK 5

RESULT 12

S33244

neuromodulatory peptide WWamide-1 - giant African snail

C;Species: Achatina fulica (giant African snail)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C;Accession: S33244

R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A;Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of

A;Reference number: S33244; PMID:93265912; PMID:8495720

A;Accession: S33244

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <MIN>

A;Cross-references: UNIPROT:P35921

Query Match

Best Local Similarity 30.3%; Score 10; DB 2; Length 7;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIS 6

Db 3 EMS 5

RESULT 13

S33245

neuromodulatory peptide WWamide-2 - giant African snail

C;Species: Achatina fulica (giant African snail)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C;Accession: S33245

R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A;Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of

A;Reference number: S33244; PMID:93265912; PMID:8495720

A;Accession: S33245

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <MIN>

A;Cross-references: UNIPROT:P35919

Query Match

Best Local Similarity 30.3%; Score 10; DB 2; Length 7;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIS 6

Db 3 EMS 5

RESULT 14

T13892

cytochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrion (frag

C;Species: mitochondrion Lampetra fluviatilis (river lamprey)

C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C;Accession: T13892

R;Delarbre, C.; Barriol, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol. 14, 807-813, 1997
A;Title: The main features of the craniate mitochondrial DNA between the ND1 and the COI
A;Reference number: Z17775; MUID:97398704; PMID:9254918
A;Accession: T13892
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-3
A;Cross-references: EMBL:Y09528; NID:g2340016; PIDN:CAA70721.1; PID:g4379123
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match 27.3%; Score 9; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
Db 2 TL 3

RESULT 15
A44955
alkanal monooxygenase (FMN-linked) (EC 1.14.14.3) alpha chain - Vibrio harveyi (fragment
C;Species: Vibrio harveyi
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-May-2000
C;Accession: A44955
R;Paquette, O.; Tu, S.C.
Photochem. Photobiol. 50, 817-825, 1989
A;Title: Chemical modification and characterization of the alpha cysteine 106 at the Vib
A;Reference number: A44955; MUID:90175700; PMID:2626493
A;Accession: A44955
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <PAQ>
C;Keywords: FMN; luminescence; monooxygenase; oxidoreductase

Query Match 27.3%; Score 9; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ISR 7
Db 3 IXR 5

Search completed: November 4, 2004, 01:24:17
Job time : 18.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:55:00 ; Search time 99.6667 Seconds
(without alignments)
40.411 Million cell updates/sec

Title: US-09-712-819D-12
Perfect score: 33
Sequence: 1 FTLEISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 167

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	42.4	7	2	P83530 lactobacill
2	13	39.4	6	1	UN06_CLOPA
3	13	39.4	6	2	P82181 spinacia ol
4	13	39.4	6	2	P82182 spinacia ol
5	11	33.3	5	1	RE31_LITRU
6	11	33.3	5	1	RE32_LITRU
7	10	30.3	7	1	E105_LITRU
8	10	30.3	7	1	WWA1_ACHFU
9	10	30.3	7	1	WWA3_ACHFU
10	9	27.3	5	1	UF01_MOUSE
11	9	27.3	7	1	CCF1_ENTFA
12	9	27.3	7	1	CHOX_ALGSP
13	9	27.3	7	1	CIA_ENTFA
14	9	27.3	7	1	GFRP_MOUSE
15	9	27.3	7	1	LANC_CARUI
16	9	27.3	7	2	P93233
17	9	27.3	7	2	O07354
18	9	27.3	7	2	O8JE81
19	8	24.2	5	1	AL14_CARMA
20	8	24.2	5	1	PSK_DAUCA
21	8	24.2	5	1	UC22_MAIZE
22	8	24.2	7	1	ALL2_CARMA
23	8	24.2	7	1	ALL3_CARMA
24	8	24.2	7	1	ALL4_CARMA
25	8	24.2	7	1	ALL5_CARMA
26	8	24.2	7	1	ALL7_CVDPO
27	8	24.2	7	1	FAR1_ASCSU
28	8	24.2	7	2	Q15903
29	8	24.2	7	2	Q8TAQ4
30	8	24.2	7	2	P70804
31	8	24.2	7	2	Q9YIQ9 human adeno

32	8	24.2	7	2	Q9YIR0
33	8	24.2	7	2	Q9YQ10
34	8	24.2	7	2	Q9YVE3
35	8	24.2	7	2	Q8JJ20
36	7	21.2	4	1	ILME_SEPOF
37	7	21.2	5	1	RE21_LITRU
38	7	21.2	6	1	ACPH_RABIT
39	7	21.2	6	1	LOK1_LOCMI
40	7	21.2	6	2	P82541
41	7	21.2	7	1	FAR2_ASCSU
42	7	21.2	7	1	UFO3_MOUSE
43	7	21.2	7	1	WWA2_ACHFU
44	7	21.2	7	2	Q15897
45	7	21.2	7	2	Q95945

Q9YIR0 human adeno
Q9YQ10 transmissib
Q9YVE3 human adeno
Q8JJ20 gallus gall
P83568 sepia offic
P82071 litoria rub
P25154 oryctolagus
P41491 locusta mig
P82541 spinacia ol
P31890 ascaris suu
P38641 mus musculu
P35920 achatina fu
Q15897 homo sapien
Q95945 saccharomyc

ALIGNMENTS

RESULT 1

P83530 PRELIMINARY; PRT; 7 AA.
ID P83530
AC P83530;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 20451;
RX PubMed=12112860;
RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
RT "High pressure effects step-wise altered protein expression in
RT Lactobacillus sanfranciscensis.";
RL Proteomics 2:765-774(2002).
CC -!- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
CC protein is: 15 kDa.
FT NON_TER 1
FT NON_TER 7
SQ SEQUENCE 7 AA; 790 MW; 6AAB02CAA731B2A0 CRC64;

Query Match 42.4%; Score 14; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLEI 5
Db 2 TLDV 5

RESULT 2

UN06_CLOPA STANDARD; PRT; 6 AA.
ID UN06_CLOPA
AC P81351;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein CP 6 from 2D-PAGE (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";

RL Electrophoresis 19:802-806(1998).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.0, its MW is: 75.9 kDa.
KW Direct protein sequencing.
FT NON TER 6
SQ SEQUENCE 6 AA; 657 MW; 605B1DC1A45A8000 CRC64;

Query Match 39.4%; Score 13; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLEI 5
Db 3 TAEI 6

RESULT 3
P82181 ID P82181 PRELIMINARY; PRT; 6 AA.
AC P82181;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 beta (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. ALVARO; TISSUE=Leaf;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 kDa.
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0019843; F:rRNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro; IPR002363; Ribosomal_L10eub.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KW Chloroplast; Ribosomal protein; rRNA-binding.
FT NON TER 6
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 39.4%; Score 13; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISR 7
Db 2 ISR 4

RESULT 5
RE31_LITRU ID RE31_LITRU STANDARD; PRT; 5 AA.
AC P82072;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAB; RANGE=1-5; NOTE=Ref.1.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
FT MOD RES 5
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 33.3%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2
Db 4 FT 5

RESULT 6
RE32_LITRU

[1]
RN SEQUENCE.
RP STRAIN=cv. ALVARO; TISSUE=Leaf;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 kDa.
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0019843; F:rRNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro; IPR002363; Ribosomal_L10eub.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KW Chloroplast; Ribosomal protein; rRNA-binding.
FT NON TER 6
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 39.4%; Score 13; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISR 7
Db 2 ISR 4

RESULT 5
RE31_LITRU ID RE31_LITRU STANDARD; PRT; 5 AA.
AC P82072;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAB; RANGE=1-5; NOTE=Ref.1.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
FT MOD RES 5
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 33.3%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2
Db 4 FT 5

RESULT 6
RE32_LITRU

ID RE32 LITRU STANDARD; PRT; 5 AA.
AC P82073;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rubellidin 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RA "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
KW Amphibian defense peptide; Direct protein sequencing.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 33.3%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2
Db 4 FT 5

RESULT 7
EI05 LITRU STANDARD; PRT; 7 AA.
ID EI05 LITRU
AC P82101;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Electrin 5.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RA "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Direct protein sequencing.
FT MOD RES 7 Alanine amide.
SQ SEQUENCE 7 AA; 834 MW; 6DD05B076B0B5030 CRC64;

Query Match 30.3%; Score 10; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIS 6
Db 5 EIA 7

RESULT 8
WWA1_ACHF

ID WWA1_ACHF STANDARD; PRT; 7 AA.
AC P35919;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE WWamide-1.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
CC -!- FUNCTION: Exhibits modulatory effects on the peripheral nervous
CC system. Inhibits activity on a central neuron.
DR PIR; S33245; S33245.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 7 Tryptophan amide.
SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 30.3%; Score 10; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIS 6
Db 3 EMS 5

RESULT 9
WWA3_ACHF STANDARD; PRT; 7 AA.
ID WWA3_ACHF
AC P35921;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE WWamide-3.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
DR PIR; S33244; S33244.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 7 Tryptophan amide.
SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 30.3%; Score 10; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIS 6
Db 3 EMS 5

RESULT 10
UF01_MOUSE STANDARD; PRT; 5 AA.
ID UF01_MOUSE
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)


```
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,
RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F., Cowthorne M.;
RL Submitted (AUG-1998) to Swiss-Prot.
CC -!- FUNCTION: Mediates tetrahydrobiopterin inhibition of GTP
CC cyclohydrolase I. This inhibition is reversed by L-phenylalanine
CC (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
DR SWISS-2DPAGE; P99025; MOUSE.
KW Direct protein sequencing.
FT INIT MET 0
FT NON TER 7
SQ SEQUENCE 7 AA; 806 MW; 71B5B057273B4700 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LEIS 6
Db 3 LLIS 6

RESULT 15
LANC_CARUI STANDARD; PRT; 7 AA.
AC P36960;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lantibiotic carnocin U149 (Fragment).
OS Carnobacterium sp. (strain U149).
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
OC Carnobacterium.
OX NCBI_TaxID=35782;
RN [1]
RP SEQUENCE.
RX MEDLINE=92321768; PubMed=1622206;
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA Nes I.F.;
RT "Purification and characterization of a new bacteriocin isolated from
RT a Carnobacterium sp.";
RL Appl. Environ. Microbiol. 58:1417-1422(1992).
CC -!- FUNCTION: Lanthionine-containing peptide antibiotic (lantibiotic).
CC Active on Gram-positive bacteria.
KW Antibiotic; Bacteriocin; Direct protein sequencing; Lantibiotic.
FT NON TER 7
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EI 5
Db 3 EI 4
```

Search completed: November 4, 2004, 01:23:17
Job time : 100.667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:54:10 ; Search time 92.3333 Seconds
(without alignments)
27.196 Million cell updates/sec

Title: US-09-712-819D-12
Perfect score: 33
Sequence: 1 FTLEISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 116873

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	72.7	7	2 AAR81848	Aar81848 Human afa
2	24	72.7	7	2 AAY41889	Aay41889 Rheumatoid
3	24	72.7	7	4 ABB55870	Abb55870 Vascular
4	24	72.7	7	4 ABB56283	Abb56283 Vascular
5	24	72.7	7	4 ABB55981	Abb55981 Vascular
6	24	72.7	7	4 AAU28602	Aau28602 DPI trypt
7	24	72.7	7	4 AAU24969	Aau24969 Schizophr
8	24	72.7	7	4 AAU26249	Aau26249 Depressio
9	24	72.7	7	4 AAU15313	Aau15313 Schizophr
10	24	72.7	7	4 ABB52190	Abb52190 Human API
11	24	72.7	7	4 ABB52355	Abb52355 Human API
12	24	72.7	7	5 ABG78901	Abg78901 Multiple
13	24	72.7	7	5 ABG78730	Abg78730 Multiple
14	24	72.7	7	6 ABP58010	Abp58010 Prostate
15	24	72.7	7	6 ABP57255	Abp57255 Breast ca
16	24	72.7	7	6 ABP57203	Abp57203 Breast ca
17	24	72.7	7	6 ABR59010	Abp59010 Alzheimer
18	24	72.7	7	6 ABR59042	Abp59042 Alzheimer
19	24	72.7	7	8 ADH35821	Adh35821 Vitamin D
20	24	72.7	7	8 ADH35827	Adh35827 Vitamin D
21	24	72.7	7	8 ADN31805	Adn31805 Human Alz
22	24	72.7	7	8 ADN32134	Adn32134 Human Alz
23	24	72.7	7	8 ADO78580	Ado78580 Schizophr
24	23	69.7	7	2 AAY40736	Aay40736 S4 deriva
25	23	69.7	7	3 AAB30074	Aab30074 Scaffold

26	22	66.7	7	2 AAY40738	Aay40738 S4 deriva
27	22	66.7	7	3 AAB30076	Aab30076 Scaffold
28	20	60.6	6	6 ABR45678	Abr45678 Staphyloc
29	20	60.6	6	6 ABR46070	Abr46070 Staphyloc
30	20	60.6	6	6 ABR46854	Abr46854 Staphyloc
31	20	60.6	6	6 ABR44950	Abr44950 Staphyloc
32	20	60.6	6	6 ABR46462	Abr46462 Staphyloc
33	20	60.6	6	6 ABR45342	Abr45342 Staphyloc
34	20	60.6	7	2 AAR07656	Aar07656 Ribonucle
35	20	60.6	7	2 AAY42013	Aay42013 Rheumatoid
36	20	60.6	7	2 AAW82668	Aaw82668 Cauliflow
37	20	60.6	7	6 ABU09135	Abu09135 Human int
38	20	60.6	7	8 ADI02925	Adi02925 Human int
39	19	57.6	6	6 ABR45118	Abr45118 Staphyloc
40	19	57.6	6	6 ABR45846	Abr45846 Staphyloc
41	19	57.6	6	6 ABR46238	Abr46238 Staphyloc
42	19	57.6	6	6 ABR46630	Abr46630 Staphyloc
43	19	57.6	6	6 ABR47022	Abr47022 Staphyloc
44	19	57.6	6	6 ABR45454	Abr45454 Staphyloc
45	19	57.6	7	2 AAR72775	Aar72775 Mammalian

ALIGNMENTS

RESULT 1
ID AAR81848 standard; peptide; 7 AA.
XX AC AAR81848;
XX DT 16-MAY-1996 (first entry)
XX DE Human afamin tryptic fragment FX20.
XX KW Human; afamin; serum protein family; albumin; alpha-foetoprotein; plasma;
KW vitamin D binding protein; homology; post-translational processing;
KW chromatography; Primer; PCR; amplification; probe; rheumatoid arthritis;
KW ischaemia-reperfusion injury; ARDS; cardiopulmonary bypass; sepsis;
XX toxic plasma substance; inflammation.
XX OS Homo sapiens.
XX PN WO9527059-A1.
XX PD 12-OCT-1995.
XX PF 31-MAR-1995; 95WO-US004075.
XX PR 31-MAR-1994; 94US-00222619.
XX PA (AMGE-) AMGEN INC.
XX PI (UYRQ) UNIV ROCKEFELLER.
XX PI Lichenstein HS, Lyons DE, Wurfel MM, Wright SD;
XX WPI; 1995-358634/46.
XX PT Human afamin or a variant and poly:nucleotide(s) encoding it - a human
PT serum protein with activities in common with other members of this
XX family.
XX PS Example 3; Page 45; 97pp; English.
XX CC Peptides AAR81847-54 are tryptic peptide fragments from human afamin
CC (AAR81845) novel member of the human serum protein family. The fragments
CC were used to design primers and probes (AAT00786-98) for the cloning of
CC the afamin gene (AAT00785) from human liver cDNA. Afamin is thought to
CC have similar properties to human albumin, alpha-foetoprotein and vitamin
CC D binding protein due to homology with these proteins. The gene encodes a
CC mature protein of 66576 daltons without post-translational processing
CC (ca. 87000 daltons with post-translational processing). The protein was
CC isolated from human plasma by a conventional chromatographic methods. The

CC	protein can be used to ameliorate ischaemia-reperfusion injury,	CC	used in the exemplification of the present invention
CC	rheumatoid arthritis, ARDS, cardiopulmonary bypass, sepsis, toxic plasma	XX	
CC	substances released after inflammation, etc	SQ	Sequence 7 AA;
XX			
SQ	Sequence 7 AA;		
	Query Match		Query Match
	Best Local Similarity 72.7%; Score 24; DB 2; Length 7;		Best Local Similarity 72.7%; Score 24; DB 2; Length 7;
	Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY	1 FTLEISR 7	QY	1 FTLEISR 7
			: :
Db	1 FTFEYSR 7	Db	1 YTFELSR 7
RESULT 2		RESULT 3	
AAAY41889		ABB55870	
ID	AAAY41889 standard; peptide; 7 AA.	ID	ABB55870 standard; peptide; 7 AA.
XX		XX	
AC	AAAY41889;	AC	ABB55870;
XX		XX	
DT	09-DEC-1999 (first entry)	DT	15-FEB-2002 (first entry)
XX		XX	
DE	Rheumatoid arthritis diagnostic protein isoform peptide #40.	DE	Vascular dementia-associated protein isoform (VPI) 70.
XX		XX	
KW	Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;	KW	Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
KW	rheumatoid arthritis diagnostic feature; ERPI; synovial fluid;	XX	diagnosis; prognosis; gene therapy.
KW	rheumatoid arthritis diagnostic protein isoform; screening;	OS	Homo sapiens.
KW	expression reference protein isoform; prognosis.	XX	
XX		XX	
OS	Homo sapiens.	PN	WO200169261-A2.
XX		XX	
PN	WO9947925-A2.	PD	20-SEP-2001.
XX		XX	
PD	23-SEP-1999.	XX	
XX		PF	14-MAR-2001; 2001WO-GB001106.
PF	15-MAR-1999; 99WO-GB0000763.	XX	
XX		PR	15-MAR-2000; 2000GB-00006285.
PR	13-MAR-1998; 98GB-00005477.	PR	24-NOV-2000; 2000GB-00028734.
XX		PR	28-NOV-2000; 2000US-00724391.
PA	(OXFO-) OXFORD GLYCOSCIENCES UK LTD.	XX	
XX		PA	(OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PI	Parekh RB, Patel TP, Townsend RR;	XX	
XX		PI	Herath HMAc, Parekh RB, Rohlf C;
DR	WPI; 1999-571871/48.	XX	WPI; 2001-557937/62.
XX		DR	
PT	Diagnosis of human rheumatoid arthritis by two-dimensional	XX	
PT	electrophoresis.	XX	
XX		XX	
PS	Disclosure; Page 18; 157pp; English.	PS	Claim 6; Page 31; 151pp; English.
XX		XX	
CC	A method has been developed for the diagnosis of human rheumatoid	CC	The invention relates to screening, diagnosis or prognosis of Vascular
CC	arthritis (RA) using two-dimensional electrophoresis to generate a two-	CC	Dementia (VD) in a subject comprising analysing body fluid from the
CC	dimensional array of features. The method can be used for screening,	CC	subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
CC	diagnosis and prognosis of RA in a subject or for monitoring the effect	CC	features containing at least one chosen feature whose relative abundance
CC	of an anti-RA drug or therapy administered to a subject. The method	CC	correlates with the presence, absence, stage or severity of VD or
CC	comprises: (a) analysing a sample of serum or plasma and optionally	CC	predicts the onset or course of VD, especially detecting in a sample of
CC	synovial fluid by two-dimensional electrophoresis, to generate a two-	CC	cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
CC	dimensional array of features; (b) identifying at least one chosen	CC	protein isoforms (VPis) (ABB55801-ABB56295) as fully defined in the
CC	feature whose relative abundance correlates with the presence or absence	CC	specification. Detecting VD-associated features and VPI is useful for the
CC	of RA; and (c) comparing the abundance of each chosen feature in the	CC	screening, diagnosis or prognosis of VD, for determining the stage or
CC	sample with the abundance of that chosen feature in serum or plasma from	CC	severity of VD, for identifying a subject at risk of VD or for monitoring
CC	one or more persons without RA, where the relative abundance of the	CC	the effect of therapy administered to a subject having VD. Nucleic acids
CC	chosen feature or features in the sample indicates the presence or	CC	encoding a VPI or inhibiting the function of a VPI are useful for the
CC	absence of RA in the subject. The method can also be used in clinical	CC	treatment of VD and for gene therapy
CC	studies for testing drugs for therapy of RA, for purification of RA-	XX	
CC	diagnostic protein isoforms (RPis), and for production of antibodies to	SQ	Sequence 7 AA;
CC	RPis. The RA-diagnostic feature (RADF) proteins can be used to identify		
CC	compounds that promote or inhibit their activity, which are then used as		
CC	RA drugs. Nucleic acid encoding RADFs can be used in gene therapy		
CC	protocols. AAAY41844 to AAAY42100 represent RPI peptides, AAAY42101 to		
CC	AAAY42103 represent expression reference protein isoform peptides and		
CC	AAZ25066 to AAZ25068 represent degenerate probes for RPis, which are all		

```
Db          1 YTFELSR 7
:| | :|||
1 YTFELSR 7

RESULT 4
ABB56283
ID ABB56283 standard; peptide; 7 AA.
XX
AC ABB56283;
XX
DT 15-FEB-2002 (first entry)
XX
DE Vascular dementia-associated protein isoform (VPI) 483.
XX
KW Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
KW diagnosis; prognosis; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200169261-A2.
XX
PD 20-SEP-2001.
XX
PF 14-MAR-2001; 2001WO-GB001106.
XX
PR 15-MAR-2000; 2000GB-00006285.
XX
PR 24-NOV-2000; 2000GB-00028734.
XX
PR 28-NOV-2000; 2000US-00724391.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAC, Parekh RB, Rohlf C;
XX
PF WPI; 2001-557937/62.
XX
PR Screening, diagnosis or prognosis of vascular dementia (VD), useful for
PT determining stage of VD and monitoring the effect of VD therapy,
PT comprises analyzing body fluid by 2-dimensional electrophoresis for
PT features correlated with VD.
XX
PS Claim 6; Page 40; 151pp; English.
XX
CC The invention relates to screening, diagnosis or prognosis of Vascular
CC Dementia (VD) in a subject comprising analysing body fluid from the
CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
CC features containing at least one chosen feature whose relative abundance
CC correlates with the presence, absence, stage or severity of VD or
CC predicts the onset or course of VD, especially detecting in a sample of
CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
CC specification. Detecting VD-associated features and VPI is useful for the
CC screening, diagnosis or prognosis of VD, for determining the stage or
CC severity of VD, for identifying a subject at risk of VD or for monitoring
CC the effect of therapy administered to a subject having VD. Nucleic acids
CC encoding a VPI or inhibiting the function of a VPI are useful for the
CC treatment of VD and for gene therapy
XX
SQ Sequence 7 AA;

Query Match 72.7%; Score 24; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db :| | :|||
1 YTFELSR 7

RESULT 5
ABB55981
ID ABB55981 standard; peptide; 7 AA.
XX
AC ABB55981;
XX
DT 03-JAN-2002 (first entry)
XX
DE DPI tryptic digest peptide #199.
XX
KW Human; depression associated protein isoform; tryptic digest peptide;
KW DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
KW maniac-depressive illness; schizoaffective disorder.
XX
```

```
XX
DT 15-FEB-2002 (first entry)
XX
DE Vascular dementia-associated protein isoform (VPI) 181.
XX
KW Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
KW diagnosis; prognosis; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200169261-A2.
XX
PD 20-SEP-2001.
XX
PF 14-MAR-2001; 2001WO-GB001106.
XX
PR 15-MAR-2000; 2000GB-00006285.
XX
PR 24-NOV-2000; 2000GB-00028734.
XX
PR 28-NOV-2000; 2000US-00724391.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAC, Parekh RB, Rohlf C;
XX
PF WPI; 2001-557937/62.
XX
PR Screening, diagnosis or prognosis of vascular dementia (VD), useful for
PT determining stage of VD and monitoring the effect of VD therapy,
PT comprises analyzing body fluid by 2-dimensional electrophoresis for
PT features correlated with VD.
XX
PS Claim 6; Page 33; 151pp; English.
XX
CC The invention relates to screening, diagnosis or prognosis of Vascular
CC Dementia (VD) in a subject comprising analysing body fluid from the
CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
CC features containing at least one chosen feature whose relative abundance
CC correlates with the presence, absence, stage or severity of VD or
CC predicts the onset or course of VD, especially detecting in a sample of
CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
CC specification. Detecting VD-associated features and VPI is useful for the
CC screening, diagnosis or prognosis of VD, for determining the stage or
CC severity of VD, for identifying a subject at risk of VD or for monitoring
CC the effect of therapy administered to a subject having VD. Nucleic acids
CC encoding a VPI or inhibiting the function of a VPI are useful for the
CC treatment of VD and for gene therapy
XX
SQ Sequence 7 AA;

Query Match 72.7%; Score 24; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db :| | :|||
1 YTFELSR 7

RESULT 6
AAU28602
ID AAU28602 standard; peptide; 7 AA.
XX
AC AAU28602;
XX
DT 03-JAN-2002 (first entry)
XX
DE DPI tryptic digest peptide #199.
XX
KW Human; depression associated protein isoform; tryptic digest peptide;
KW DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
KW maniac-depressive illness; schizoaffective disorder.
XX
```

XX OS Homo sapiens.
XX PN WO200162787-A1.
XX PD 30-AUG-2001.
XX PF 23-FEB-2001; 2001WO-GB0000786.
XX PR 24-FEB-2000; 2000GB-00004412.
XX PR 08-DEC-2000; 2000GB-00030050.
XX PR 12-DEC-2000; 2000US-0254830P.
XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX PI Herath HMAc, Parekh RB, Rohlf C, Terrett JA, Tyson KL;
XX DR WPI; 2001-570626/64.
XX PT Novel nucleic acid encoding a protein associated with bipolar affective disorder, which is used for diagnosis, prophylaxis and therapy of neuropsychiatric disorders, such as bipolar affective disorder.
XX PS Disclosure; Page 34; 153pp; English.
XX CC The present invention relates to the identification of depression associated protein isoforms (DPIs), particularly the tryptic digest peptides of these proteins. Some of the DPIs (AAU28404-AAU28625) described are decreased in the cerebrospinal fluid (CSF) of BAD (bipolar affective disorder) subjects, whilst other DPIs (AAU28626-AAU28887) are increased in BAD subjects. Also described are peptide sequences identified from DPI-45 and DPI-213 and the nucleic acid sequence they are encoded by. The sequences of the invention are useful for clinical screening, diagnosis, prognosis, therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder, BP), manic-depressive illnesses, attention deficit disorders, schizoaffective disorders, and unipolar affective disorders. The present sequence represents one of the DPI tryptic digest peptides of the present invention
XX SQ Sequence 7 AA;
Query Match 72.7%; Score 24; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 FTLEISR 7
:|:|:
Db 1 YTFELSR 7
RESULT 7
AAU24969
ID AAU24969 standard; peptide; 7 AA.
XX AC AAU24969;
XX DT 18-DEC-2001 (first entry)
XX DE Schizophrenia-Associated Protein Isoform (SPI) peptide #198.
XX DE Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240; neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
XX KW Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240; neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
XX OS Homo sapiens.
XX OS WO200162785-A2.
XX PN 30-AUG-2001.
XX PD 23-FEB-2001; 2001WO-GB0000792.
XX PF 24-FEB-2000; 2000GB-00004415.
PR

PR 28-DEC-2000; 2000US-00750395.
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX PI Herath HMAc, Parekh RB, Rohlf C, Terrett JA, Tyson KL;
XX DR WPI; 2001-570624/64.
XX PT New schizophrenia associated protein isoforms and encoding nucleic acid molecules, useful for treatment, diagnosis and prognosis of schizophrenia and screening for potential drugs for treatment and new drug targets.
XX PS Disclosure; Page 32; 148pp; English.
XX CC The sequence represents a schizophrenia-associated protein isoform (SPI). These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable in cerebrospinal fluid, serum or plasma and are useful markers of schizophrenia. The sequences can be used for treatment and diagnosis of schizophrenia, screening, prognosis, monitoring the results of therapy, identifying patients most likely to respond to a particular therapy and identification of new targets for drug treatment. SPI DNA is useful as a nucleic acid probe to detect the presence of nucleic acids or SPIs
XX SQ Sequence 7 AA;
Query Match 72.7%; Score 24; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 FTLEISR 7
:|:|:
Db 1 YTFELSR 7
RESULT 8
AAU26249
ID AAU26249 standard; peptide; 7 AA.
XX AC AAU26249;
XX DT 18-DEC-2001 (first entry)
XX DE Depression-Associated Protein isoform DPI-208.
XX DE Human; Bipolar Affective Disorder; BAD; Depression-Associated feature; DF; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid; CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic; attention deficient disorder; schizoaffective disorder; unipolar affective disorder.
XX OS Homo sapiens.
XX PN WO200163294-A2.
XX PD 30-AUG-2001.
XX PF 23-FEB-2001; 2001WO-GB0000791.
XX PR 24-FEB-2000; 2000GB-00004412.
XX PR 08-DEC-2000; 2000GB-00030050.
XX PR 12-DEC-2000; 2000US-0254830P.
XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX PI Herath HMAc, Parekh RB, Rohlf C;
XX DR WPI; 2001-582081/65.
XX PT Preparation for diagnosing or treating bipolar affected disorder (BAD) or unipolar depression, or for screening for modulators, comprises a BAD-associated protein isoform.
XX PS Claim 8; Page 34; 163pp; English.

XX The invention relates to a preparation comprising an isolated Bipolar
CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPIs are
CC used to screen, diagnose or prognosis of BAD or unipolar depression,
CC determine the stage or severity of BAD or unipolar depression, identify a
CC subject at risk of developing BAD or unipolar depression, or monitor the
CC effect of therapy in a subject. They are also used to screen for or
CC identify agents that interact with a DPI. These agents, antibodies
CC against the DPIs, and nucleic acids encoding the DPIs are used to treat
CC or prevent BAD or unipolar depression. Diseases that can be treated are
CC attention deficient disorder, a schizoaffective disorder, a bipolar or a
CC unipolar affective disorder. The DPIs are used in proteomics. The
CC proteomic approach of using DPIs for screening, diagnosis or prognosis of
CC BAD or unipolar depression overcomes the problems of using gene
CC expression analysis, such as not being able to obtain central nervous
CC system (CNS) tissue from a living patient under normal circumstances. The
CC present sequence is a DIP decreased in the CSF (cerebro-spinal fluid) of
CC subjects having BAD
XX

SQ Sequence 7 AA;

Query Match 72.7%; Score 24; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7
:|:|:
Db 1 YTFELSR 7

RESULT 9
AAU15313
ID AAU15313 standard; peptide; 7 AA.
XX
AC AAU15313;
XX

DT 24-OCT-2001 (first entry)

DE Schizophrenia-associated isoform peptide #199.

XX Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;
KW neurological disorder; neuropathy.
KW

OS Homo sapiens.

XX WO200163293-A2.

PN 30-AUG-2001.

PD 23-FEB-2001; 2001WO-GB000783.

PF 24-FEB-2000; 2000GB-00004415.

PR 28-DEC-2000; 2000US-00750395.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PA Herath HMAc, Parekh RB, Rohlf C;

XX WPI; 2001-502868/55.

PI Diagnosing and monitoring Schizophrenia by detecting the presence of
XX Schizophrenia Associated Features and Schizophrenia Associated Protein
PT Isoforms in samples of cerebrospinal fluid.
PT

XX Claim 6; Page 32; 160pp; English.

PS The invention relates to methods and compositions for screening,
XX diagnosis and prognosis of Schizophrenia. The method involves detecting
CC the presence of Schizophrenia (SCH) Associated Features (SFs) and SCH
CC Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis,
CC immunoassay or hybridisation assay, for diagnosing and monitoring SCH,
CC studying the effectiveness of treatments and for identifying potential
CC therapeutic agents. The method is used for (1) screening or diagnosis of

CC SCH and the relative abundance of at least 1 chosen feature correlates
CC with the presence or absence of SCH; and (2) monitoring the effect of
CC therapy administered to a subject with SCH and the relative abundance of
CC at least 1 chosen feature which correlates with the severity of SCH. The
CC expression and activity of the SFs, SPIs and related molecules (e.g.
CC secondary messengers) are studied to diagnose SCH, monitor the progress
CC of the disorder and the effectiveness of treatment and as targets to
CC identify and produce potential therapeutic agents for the treatment of
CC SCH. The paucity of detectable neurologic defects distinguishes
CC neuropsychiatric disorders such as SCH from neurological disorders, where
CC manifestations of anatomical and biochemical changes have been identified
CC in many cases. Consequently the identification and characterisation of
CC cellular and/or molecular causative defects and neuropathies are
CC necessary for improved treatment of neuropsychiatric disorders. AAU15114-
CC AAU15762 represent the amino acid sequences of schizophrenia-associated
CC isoforms used in the method of the invention
XX

SQ Sequence 7 AA;

Query Match 72.7%; Score 24; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7
:|:|:
Db 1 YTFELSR 7

RESULT 10
ABB52190
ID ABB52190 standard; peptide; 7 AA.
XX
AC ABB52190;
XX

DT 08-FEB-2002 (first entry)

DE Human API-146 tryptic digest peptide #1.

XX Human; neuroprotective; nootropic; gene therapy; vaccine;
KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
KW Expression Reference Protein Isoform; ERPI; proteolysis.

OS Homo sapiens.

XX WO200175454-A2.

PN 11-OCT-2001.

PD 03-APR-2001; 2001WO-US010908.

PF 03-APR-2000; 2000US-0194504P.

PR 28-NOV-2000; 2000US-0253647P.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PA (PFIZ) PFIZER INC.

XX Durham KL, Friedman DL, Herath HMAc, Kimmel LH, Parekh RB;

PI Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;

XX Townsend RR, White F, Williams SA;

XX WPI; 2001-639384/73.

XX Screening for Alzheimer's disease in a mammal, by making two-dimensional
PT array of a feature whose relative abundance correlates with disease, and
PT comparing with abundance of the feature in samples of healthy persons.

XX Example; Page 30; 162pp; English.

PS The invention relates to methods for the screening, diagnosis and
XX prognosis of Alzheimer's disease. The methods involve the detection of
CC Alzheimer's Disease-Associated Features (AFs) and Alzheimer's Disease-
CC Associated Protein Isoforms (APIs) in cerebrospinal fluid, serum or

CC plasma. The abundance of the Afs and APIs is then normalised to an
CC Expression Reference Protein Isoform (ERPI) in order to determine whether
CC a patient is suffering from, or has a predisposition to, Alzheimer's
CC Disease. The relative abundance of the Afs and APIs correlates with the
CC severity of Alzheimer's Disease. The present sequence is a peptide
CC produced from an API by proteolysis

XX
SQ Sequence 7 AA;

Query Match 72.7%; Score 24; DB 4; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 1 FTFEYSR 7

RESULT 11
ABB52355
ID ABB52355 standard; peptide; 7 AA.
XX
AC ABB52355;
XX
DT 08-FEB-2002 (first entry)
XX
DE Human API-125 tryptic digest peptide #8.
XX
KW Human; neuroprotective; nootropic; gene therapy; vaccine;
KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
KW Expression Reference Protein Isoform; ERPI; proteolysis.
XX
OS Homo sapiens.
XX
PN WO200175454-A2.
XX
PD 11-OCT-2001.
XX
PF 03-APR-2001; 2001WO-US010908.
XX
PR 03-APR-2000; 2000US-0194504P.
PR 28-NOV-2000; 2000US-0253647P.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA (PFIZ) PFIZER INC.
XX
PI Durham KL, Friedman DL, Herath HMAc, Kimmel LH, Parekh RB;
PI Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;
PI Townsend RR, White F, Williams SA;
XX
DR WPI; 2001-639384/73.
XX
PT Screening for Alzheimer's disease in a mammal, by making two-dimensional
PT array of a feature whose relative abundance correlates with disease, and
PT comparing with abundance of the feature in samples of healthy persons.
XX
PS Example; Page 34; 162pp; English.
XX
CC The invention relates to methods for the screening, diagnosis and
CC prognosis of Alzheimer's disease. The methods involve the detection of
CC Alzheimer's Disease-Associated Features (AFs) and Alzheimer's Disease-
CC Associated Protein Isoforms (APIs) in cerebrospinal fluid, serum or
CC plasma. The abundance of the Afs and APIs is then normalised to an
CC Expression Reference Protein Isoform (ERPI) in order to determine whether
CC a patient is suffering from, or has a predisposition to, Alzheimer's
CC Disease. The relative abundance of the Afs and APIs correlates with the
CC severity of Alzheimer's Disease. The present sequence is a peptide
CC produced from an API by proteolysis

XX
SQ Sequence 7 AA;

Query Match 72.7%; Score 24; DB 4; Length 7;

Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 1 YTFELSR 7

RESULT 12
ABG78901
ID ABG78901 standard; peptide; 7 AA.
XX
AC ABG78901;
XX
DT 29-NOV-2002 (first entry)
XX
DE Multiple sclerosis associated feature (MSF) tryptic digest peptide #389.
XX
KW Multiple sclerosis; MS; multiple sclerosis associated feature; MSAF;
KW human; multiple sclerosis-associated protein isoform; MSPI;
KW antiinflammatory; neuroprotective.
XX
OS Homo sapiens.
XX
PN WO200259604-A2.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-GB000330.
XX
PR 26-JAN-2001; 2001US-0264404P.
PR 20-NOV-2001; 2001US-0331647P.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAc, Parekh RB, Rohlf C;
XX
DR WPI; 2002-599812/64.
XX
PT Screening or diagnosing multiple sclerosis (MS), useful for e.g.
PT determining the stage or severity of MS, comprises detecting the presence
PT of MS-associated features or protein isoforms by 2-dimensional
PT electrophoresis.
XX
PS Disclosure; Page 39; 128pp; English.
XX
CC This invention relates to a novel method for screening or diagnosing
CC multiple sclerosis (MS) in a subject to determine the stage or severity
CC of MS, to identify a subject at risk of developing MS or to monitor the
CC effect of a therapy administered. The method comprises analysing a sample
CC body fluid from the subject by two-dimensional electrophoresis and
CC detecting the presence of multiple sclerosis-associated features (MSFs),
CC or multiple sclerosis-associated protein isoforms (MSPIs). The MSF's of
CC the invention correspond to spots identified on a 2D gel these proteins
CC may have antiinflammatory or neuroprotective activity. The methods of the
CC invention and the compositions are useful for clinical screening,
CC diagnosis and treatment of MS, for monitoring the effectiveness of MS
CC treatment, for selecting participants in clinical trials, for identifying
CC patients most likely to respond to a particular therapeutic treatment and
CC for screening and developing drugs for treatment of MS. Agents that
CC modulate the expression or activity of an MSPI are useful for treating
CC MS, for preventing or delaying the onset or development of MS, to prevent
CC or delay the progression of MS, or to ameliorate the symptoms MS. Nucleic
CC acids comprising a sequence encoding an MSPI, MSPI-related polypeptide,
CC or their fragments are useful for promoting MSPI function by gene
CC therapy. The present sequence represents a human multiple sclerosis
CC associated feature tryptic digest peptide of the invention

XX
SQ Sequence 7 AA;

Query Match 72.7%; Score 24; DB 5; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7 :| | :| |
Db 1 YTFELSR 7

RESULT 13
ABG78730
ID ABG78730 standard; peptide; 7 AA.
XX
AC ABG78730;
XX
DT 29-NOV-2002 (first entry)
XX
DE Multiple sclerosis associated feature (MSF) tryptic digest peptide #218.
XX
KW Multiple sclerosis; MS; multiple sclerosis associated feature; MSAF;
KW human; multiple sclerosis-associated protein isoform; MSPI;
KW antiinflammatory; neuroprotective.
XX
OS Homo sapiens.
XX
PN WO200259604-A2.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-GB000330.
XX
PR 26-JAN-2001; 2001US-0264404P.
XX
PR 20-NOV-2001; 2001US-0331647P.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAC, Parekh RB, Rohlf C;
XX
DR WPI; 2002-599812/64.
XX
PT Screening or diagnosing multiple sclerosis (MS), useful for e.g.
PT determining the stage or severity of MS, comprises detecting the presence
PT of MS-associated features or protein isoforms by 2-dimensional
PT electrophoresis.
XX
PS Disclosure; Page 26; 128pp; English.
XX
CC This invention relates to a novel method for screening or diagnosing
CC multiple sclerosis (MS) in a subject to determine the stage or severity
CC of MS, to identify a subject at risk of developing MS or to monitor the
CC effect of a therapy administered. The method comprises analysing a sample
CC body fluid from the subject by two-dimensional electrophoresis and
CC detecting the presence of multiple sclerosis-associated features (MSFs),
CC or multiple sclerosis-associated protein isoforms (MSPIs). The MSF's of
CC the invention correspond to spots identified on a 2D gel these proteins
CC may have antiinflammatory or neuroprotective activity. The methods of the
CC invention and the compositions are useful for clinical screening,
CC diagnosis and treatment of MS, for monitoring the effectiveness of MS
CC treatment, for selecting participants in clinical trials, for identifying
CC patients most likely to respond to a particular therapeutic treatment and
CC for screening and developing drugs for treatment of MS. Agents that
CC modulate the expression or activity of an MSPI are useful for treating
CC MS, for preventing or delaying the onset or development of MS, to prevent
CC or delay the progression of MS, or to ameliorate the symptoms MS. Nucleic
CC acids comprising a sequence encoding an MSPI, MSPI-related polypeptide,
CC or their fragments are useful for promoting MSPI function by gene
CC therapy. The present sequence represents a human multiple sclerosis
CC associated feature tryptic digest peptide of the invention
XX
SQ Sequence 7 AA;

Query Match 72.7%; Score 24; DB 5; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7 :| | :| |
Db 1 YTFELSR 7

RESULT 14
ABP58010
ID ABP58010 standard; peptide; 7 AA.
XX
AC ABP58010;
XX
DT 11-FEB-2003 (first entry)
XX
DE Prostate cancer marker protein peptide fragment.
XX
KW Prostate cancer; marker; vitamin D binding protein; VDBP; human;
KW diagnosis; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200275314-A2.
XX
PD 26-SEP-2002.
XX
PF 30-NOV-2001; 2001WO-US045031.
XX
PR 30-NOV-2000; 2000US-0250284P.
XX
PR 08-NOV-2001; 2001US-0344948P.
XX
PA (MATR-) MATRITECH INC.
XX
PI Hlavaty J, Briggman JV;
XX
DR WPI; 2003-067369/06.
XX
PT Diagnosing or treating prostate cancer by detecting in a sample isolated
PT from the individual the presence of prostate cancer-associated protein.
XX
PS Claim 1; Page 41; 63pp; English.
XX
CC The present sequence is that of a peptide fragment of a novel human 50.8
CC kDa prostate cancer-associated protein that has been identified as a
CC highly effective marker for prostate cancer. The novel protein includes a
CC polypeptide that is related to human serum vitamin D binding protein
CC (VDBP, see ABP58017). The present peptide corresponds to amino acids 346-
CC 352 of this VDBP allele. It is one of a series of peptides (see ABP58005-
CC 16) that distinguish VDBP-related proteins from other proteins, or which
CC may be characterised as binding specifically to an anti-VDBP antibody.
CC VDBP-related proteins are detectable at a higher concentration in serum
CC from a mammal, e.g. a human, with prostate cancer relative to serum from
CC a healthy mammal and can therefore be used as prostate cancer markers.
CC They permit the rapid detection, preferably before metastases occur, of
CC prostate cancer. A target prostate cancer-associated protein may be
CC detected using a labelled antibody capable of binding specifically to the
CC protein. Prostate cancer-associated proteins, and nucleic acids encoding
CC them, are also useful as targets for treating prostate cancer, and as
CC indicators for monitoring the efficiency of prostate cancer therapy
XX
SQ Sequence 7 AA;

Query Match 72.7%; Score 24; DB 6; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7 :| | :| |
Db 1 YTFELSR 7

RESULT 15
ABP57255
ID ABP57255 standard; peptide; 7 AA.
XX
AC ABP57255;

Db 1 YTFELSR 7 :| | :| |

RESULT 14
ABP58010
ID ABP58010 standard; peptide; 7 AA.
XX
AC ABP58010;
XX
DT 11-FEB-2003 (first entry)
XX
DE Prostate cancer marker protein peptide fragment.
XX
KW Prostate cancer; marker; vitamin D binding protein; VDBP; human;
KW diagnosis; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200275314-A2.
XX
PD 26-SEP-2002.
XX
PF 30-NOV-2001; 2001WO-US045031.
XX
PR 30-NOV-2000; 2000US-0250284P.
XX
PR 08-NOV-2001; 2001US-0344948P.
XX
PA (MATR-) MATRITECH INC.
XX
PI Hlavaty J, Briggman JV;
XX
DR WPI; 2003-067369/06.
XX
PT Diagnosing or treating prostate cancer by detecting in a sample isolated
PT from the individual the presence of prostate cancer-associated protein.
XX
PS Claim 1; Page 41; 63pp; English.
XX
CC The present sequence is that of a peptide fragment of a novel human 50.8
CC kDa prostate cancer-associated protein that has been identified as a
CC highly effective marker for prostate cancer. The novel protein includes a
CC polypeptide that is related to human serum vitamin D binding protein
CC (VDBP, see ABP58017). The present peptide corresponds to amino acids 346-
CC 352 of this VDBP allele. It is one of a series of peptides (see ABP58005-
CC 16) that distinguish VDBP-related proteins from other proteins, or which
CC may be characterised as binding specifically to an anti-VDBP antibody.
CC VDBP-related proteins are detectable at a higher concentration in serum
CC from a mammal, e.g. a human, with prostate cancer relative to serum from
CC a healthy mammal and can therefore be used as prostate cancer markers.
CC They permit the rapid detection, preferably before metastases occur, of
CC prostate cancer. A target prostate cancer-associated protein may be
CC detected using a labelled antibody capable of binding specifically to the
CC protein. Prostate cancer-associated proteins, and nucleic acids encoding
CC them, are also useful as targets for treating prostate cancer, and as
CC indicators for monitoring the efficiency of prostate cancer therapy
XX
SQ Sequence 7 AA;

Query Match 72.7%; Score 24; DB 6; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7 :| | :| |
Db 1 YTFELSR 7

RESULT 15
ABP57255
ID ABP57255 standard; peptide; 7 AA.
XX
AC ABP57255;

[illegible]

16-APR-2003	(first entry)
Breast cancer associated tryptic digest peptide SEQ ID NO:154.	
Breast cancer associated feature; BF; BPI; breast cancer; diagnosis; breast cancer associated protein isoform; cytostatic; gene therapy.	
Homo sapiens.	
Synthetic.	
WO200288750-A2.	
07-NOV-2002.	
02-MAY-2002; 2002WO-GB002022.	
02-MAY-2001; 2001GB-00010790.	
27-JUL-2001; 2001GB-00018385.	
14-AUG-2001; 2001GB-00019791.	
16-AUG-2001; 2001GB-00020045.	
22-NOV-2001; 2001GB-00028062.	
(OXFO-) OXFORD GLYCOSCIENCES UK LTD.	
Herath HMAC;	
WPI; 2003-175048/17.	
Screening, diagnosing or determining the stage or severity of breast cancer, comprises analyzing and quantitatively detecting Breast Cancer-Associated Features or Breast Cancer-Associated Protein Isoforms in a biological sample.	
Example; Page 77; 88pp; English.	
The present invention describes a method for screening, diagnosing or determining the stage or severity of breast cancer, identifying a subject at risk of developing breast cancer, or monitoring the effect of therapy administered to a subject with breast cancer, by generating a two-dimensional array of features comprising breast cancer-associated features (BFs), or quantitatively detecting breast cancer-associated protein isoforms (BPIs). Also described: (1) an antibody capable of immunospecifically binding to one of the BPIs; (2) a pharmaceutical compositions comprising: (a) a BPI, or a nucleic acid encoding a BPI, and a carrier; or (b) the antibody of (1), or a fragment or derivative of the antibody, and a carrier; (3) screening for agents that interact with one or more BPIs, BPI fragments, polypeptides related to BPIs, or BPI-fusion proteins; (4) screening for or identifying agents that modulate the expression or activity of one or more BPIs, a BPI fragment, a BPI-related polypeptide, or BPI-fusion proteins; and (5) treating or preventing breast cancer. BPIs have cytostatic activity and can be used in gene therapy. Methods and kits comprising antibodies or the BPIs from the present invention can be used for screening, diagnosing or determining the stage or severity of breast cancer, identifying a subject at risk of developing breast cancer, or monitoring the effect of therapy administered to a subject with breast cancer. The antibodies, BPIs, nucleic acids encoding the BPIs, or an agent that modulates the activity of one or more BPIs are useful for treating or preventing breast cancer. ABP57104 to ABP57250 represent breast cancer associated tryptic digest peptides, which are used in the exemplification of the present invention	
Sequence 7 AA;	
Query Match	72.7%; Score 24; DB 6; Length 7;
Best Local Similarity	57.1%; Pred. No. 1.7e+06;
Matches 4: Conservative	2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTLEISR 7
:|:|
Dp 1 YTFELSR 7

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OM protein - protein search, using sw model

Run on: November 4, 2004, 01:23:27 ; Search time 69.3333 Seconds
(without alignments)
32.733 Million cell updates/sec

Title: US-09-712-819D-12

Perfect score: 33

Sequence: 1 FTLEISR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 56143

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:

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19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	72.7	7	9	US-09-791-378-198
2	24	72.7	7	9	US-09-998-909-7
3	24	72.7	7	9	US-09-826-290-205
4	24	72.7	7	9	US-09-826-290-370
5	24	72.7	7	10	US-09-791-393-145
6	24	72.7	7	10	US-09-791-389-145
7	24	72.7	7	11	US-09-791-377-198
8	24	72.7	7	15	US-10-264-309-131
9	24	72.7	7	15	US-10-264-309-460
10	24	72.7	7	15	US-10-601-100-105
11	24	72.7	7	17	US-10-700-340-52
12	24	72.7	7	17	US-10-700-340-154
13	20	60.6	7	13	US-10-050-552A-4
					Sequence 198, App
					Sequence 7, Appli
					Sequence 205, App
					Sequence 370, App
					Sequence 145, App
					Sequence 145, App
					Sequence 198, App
					Sequence 131, App
					Sequence 460, App
					Sequence 105, App
					Sequence 52, Appl
					Sequence 154, App
					Sequence 4, Appli

14	20	60.6	7	14	US-10-234-026-6	Sequence 6, Appli
15	20	60.6	7	15	US-10-238-965-4	Sequence 4, Appli
16	18	54.5	5	16	US-10-803-622-3	Sequence 3, Appli
17	18	54.5	5	16	US-10-803-653-3	Sequence 3, Appli
18	18	54.5	6	9	US-09-876-388-6	Sequence 6, Appli
19	18	54.5	6	14	US-10-105-930-39	Sequence 39, Appl
20	18	54.5	6	14	US-10-287-892-6	Sequence 6, Appli
21	18	54.5	6	14	US-10-288-340-6	Sequence 6, Appli
22	18	54.5	6	16	US-10-722-733-6	Sequence 6, Appli
23	18	54.5	6	16	US-10-723-099-6	Sequence 6, Appli
24	18	54.5	6	16	US-10-803-622-197	Sequence 197, App
25	18	54.5	6	16	US-10-803-653-197	Sequence 197, App
26	18	54.5	7	9	US-09-772-105-23	Sequence 23, Appl
27	18	54.5	7	9	US-09-876-388-7	Sequence 7, Appli
28	18	54.5	7	14	US-10-287-892-7	Sequence 7, Appli
29	18	54.5	7	14	US-10-288-340-7	Sequence 7, Appli
30	18	54.5	7	16	US-10-722-733-7	Sequence 7, Appli
31	18	54.5	7	16	US-10-723-099-7	Sequence 7, Appli
32	17	51.5	6	9	US-09-727-963A-38	Sequence 38, Appl
33	17	51.5	6	14	US-10-006-869-636	Sequence 636, App
34	17	51.5	6	14	US-10-006-869-650	Sequence 650, App
35	17	51.5	6	14	US-10-020-354-101	Sequence 101, App
36	17	51.5	6	14	US-10-395-032-636	Sequence 636, App
37	17	51.5	6	14	US-10-395-032-650	Sequence 650, App
38	17	51.5	6	15	US-10-328-953-42	Sequence 42, Appl
39	17	51.5	6	15	US-10-367-580-312	Sequence 312, App
40	17	51.5	6	15	US-10-367-593-312	Sequence 312, App
41	17	51.5	6	15	US-10-367-594-312	Sequence 312, App
42	17	51.5	6	15	US-10-367-654-312	Sequence 312, App
43	17	51.5	6	15	US-10-367-658-312	Sequence 312, App
44	17	51.5	6	15	US-10-367-668-312	Sequence 312, App
45	17	51.5	6	16	US-10-367-674-312	Sequence 312, App

ALIGNMENTS

RESULT 1
US-09-791-378-198
; Sequence 198, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF SCHIZOPHRENIA
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791,378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 198
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-198

Query Match 72.7%; Score 24; DB 9; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTLEISR 7
:|:|:
Db 1 YTFELSR 7

RESULT 2
US-09-998-909-7
; Sequence 7, Application US/09998909
; Patent No. US20020164664A1
; GENERAL INFORMATION:
; APPLICANT: Hlavaty, John

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; APPLICANT: Briggman, Joseph
; TITLE OF INVENTION: Detection and Treatment of Prostate Cancer
; FILE REFERENCE: MTP-027
; CURRENT APPLICATION NUMBER: US/09/998,909
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/250,284
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-998-909-7

Query Match          72.7%; Score 24; DB 9; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FTLEISR 7
      :| | |
Db      1 YTFELSR 7

RESULT 3
US-09-826-290-205
; Sequence 205, Application US/09826290
; Patent No. US20020164668A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L.Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlff, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 370
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-370

Query Match          72.7%; Score 24; DB 9; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FTLEISR 7
      :| | |
Db      1 YTFELSR 7

RESULT 5
US-09-791-393-145
; Sequence 145, Application US/09791393
; Publication No. US20030032200A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlff, Christian
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-393-145

Query Match          72.7%; Score 24; DB 10; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FTLEISR 7
      :| | |
Db      1 FTFEYSR 7

RESULT 4
US-09-826-290-370
; Sequence 370, Application US/09826290
; Patent No. US20020164668A1
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QY 1 FTLEISR 7
:|:|:
Db 1 YTFELSR 7

RESULT 6

US-09-791-389-145
; Sequence 145, Application US/09791389
; Publication No. US20030032773A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohiff, Christian
; APPLICANT: Terrett, Jonathan Alexander
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/791,389
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GB 0004412.3
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GB 0030050.9
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/254,830
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-389-145

Query Match 72.7%; Score 24; DB 10; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7
:|:|:
Db 1 YTFELSR 7

RESULT 7

US-09-791-377-198
; Sequence 198, Application US/09791377
; Publication No. US20040110938A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-060-999
; CURRENT APPLICATION NUMBER: US/09/791,377
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 198
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-377-198

Query Match 72.7%; Score 24; DB 11; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7
:|:|:
Db 1 YTFELSR 7

RESULT 8

US-10-264-309-131
; Sequence 131, Application US/10264309
; Publication No. US20040022794A1
; GENERAL INFORMATION:
; APPLICANT: DURHAM, L. KATHRYN
; APPLICANT: FRIEDMAN, DAVID L.
; APPLICANT: HERATH, HERATH
; APPLICANT: KIMMEL, LIDA H.
; APPLICANT: PAREKH, RAJESH B.
; APPLICANT: POTTER, DAVID M.
; APPLICANT: ROHLFF, CHRISTIAN
; APPLICANT: SILBER, B. MICHAEL
; APPLICANT: SNYDER, PETER J.
; APPLICANT: SOARES, HOLLY D.
; APPLICANT: STIGER, THOMAS R.
; APPLICANT: SUNDERLAND, P. TREY
; APPLICANT: TOWNSEND, ROBERT R.
; APPLICANT: WHITE, W. FROST
; APPLICANT: WILLIAMS, STEPHEN A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
; TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
; FILE REFERENCE: POA-002.01
; CURRENT APPLICATION NUMBER: US/10/264,309
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: 60/326,708
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 131
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-309-131

Query Match 72.7%; Score 24; DB 15; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTLEISR 7
:|:|:
Db 1 FTFEYSR 7

RESULT 9

US-10-264-309-460
; Sequence 460, Application US/10264309
; Publication No. US20040022794A1
; GENERAL INFORMATION:
; APPLICANT: DURHAM, L. KATHRYN
; APPLICANT: FRIEDMAN, DAVID L.
; APPLICANT: HERATH, HERATH
; APPLICANT: KIMMEL, LIDA H.
; APPLICANT: PAREKH, RAJESH B.
; APPLICANT: POTTER, DAVID M.
; APPLICANT: ROHLFF, CHRISTIAN
; APPLICANT: SILBER, B. MICHAEL
; APPLICANT: SNYDER, PETER J.
; APPLICANT: SOARES, HOLLY D.
; APPLICANT: STIGER, THOMAS R.
; APPLICANT: SUNDERLAND, P. TREY
; APPLICANT: TOWNSEND, ROBERT R.
; APPLICANT: WHITE, W. FROST
; APPLICANT: WILLIAMS, STEPHEN A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
; TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
; FILE REFERENCE: POA-002.01
; CURRENT APPLICATION NUMBER: US/10/264,309
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: 60/326,708
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 491

; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 460
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-309-460

Query Match 72.7%; Score 24; DB 15; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7
:|:|:
Db 1 YTFELSR 7

RESULT 10
US-10-601-100-105
; Sequence 105, Application US/10601100
; Publication No. US20040072261A1
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: Method for the Diagnosis and Differential Diagnosis of
; TITLE OF INVENTION: Neurological Diseases
; FILE REFERENCE: 11362.0038.NPUS01
; CURRENT APPLICATION NUMBER: US/10/601,100
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: EP 02447121.1
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/396,437
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 105
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-601-100-105

Query Match 72.7%; Score 24; DB 15; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7
:|:|:
Db 1 YTFELSR 7

RESULT 11
US-10-700-340-52
; Sequence 52, Application US/10700340
; Publication No. US20040203023A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF BREAST
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 2543-1-032
; CURRENT APPLICATION NUMBER: US/10/700,340
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: PCT/GB02/02022
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: GB0110790.3
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: GB0118385.4
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: GB0119791.2
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB0120045.0
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: GB0128062.7
; PRIOR FILING DATE: 2001-11-22
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 52
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-700-340-52

Query Match 72.7%; Score 24; DB 17; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTLEISR 7
:|:|:
Db 1 FTFEYSR 7

RESULT 12
US-10-700-340-154
; Sequence 154, Application US/10700340
; Publication No. US20040203023A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF BREAST
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 2543-1-032
; CURRENT APPLICATION NUMBER: US/10/700,340
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: PCT/GB02/02022
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: GB0110790.3
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: GB0118385.4
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: GB0119791.2
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB0120045.0
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: GB0128062.7
; PRIOR FILING DATE: 2001-11-22
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 154
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-700-340-154

Query Match 72.7%; Score 24; DB 17; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7
:|:|:
Db 1 YTFELSR 7

RESULT 13
US-10-050-552A-4
; Sequence 4, Application US/10050552A
; Publication No. US20020187512A1
; GENERAL INFORMATION:
; APPLICANT: Nagem, Ronaldo A.P.
; APPLICANT: Colau, Didier
; APPLICANT: Renauld, Jean-Christophe
; APPLICANT: Dumoutier, Laure
; APPLICANT: Polikarpov, Igor
; TITLE OF INVENTION: Crystal Structure of Interleukin-22
; FILE REFERENCE: LUD-5722 US
; CURRENT APPLICATION NUMBER: US/10/050,552A
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/317,937
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/333,150
; PRIOR FILING DATE: 2001-11-27

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; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: A conserved sequence between Region 2 in IL-22 and IL-10
US-10-050-552A-4

Query Match          60.6%; Score 20; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FILE 4
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Db      1 FILE 4

RESULT 14
US-10-234-026-6
; Sequence 6, Application US/10234026
; Publication No. US20030097679A1
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnol
; APPLICANT: Guy Jerome Corneel Bauw
; APPLICANT: Mark William Davey
; APPLICANT: Jens Ostergaard
; APPLICANT: Marc Charles Ernest Van Montagu
; TITLE OF INVENTION: PRODUCTION OF ASCORBIC ACID IN PLANTS
; FILE REFERENCE: DECLES.001C1
; CURRENT APPLICATION NUMBER: US/10/234,026
; CURRENT FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: NL 1006000
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: PCT/EP98/02830
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 09/423,468
; PRIOR FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Brassica oleracea
US-10-234-026-6

Query Match          60.6%; Score 20; DB 14; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 TLEISR 7
      |:|:|:
Db      2 TIELSK 7

RESULT 15
US-10-238-965-4
; Sequence 4, Application US/10238965
; Publication No. US20040002586A1
; GENERAL INFORMATION:
; APPLICANT: Nagem, Ronaldo A.P.
; APPLICANT: Colau, Didier
; APPLICANT: Renauld, Jean-Christophe
; APPLICANT: Dumoutier, Laure
; APPLICANT: Polikarpov, Igor
; TITLE OF INVENTION: Crystal Structure of Interleukin-22
; FILE REFERENCE: LUD-5722 US
; CURRENT APPLICATION NUMBER: US/10/238,965
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/317,937
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/333,150

; PRIOR FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: A conserved sequence between Region 2 in IL-22 and IL-10
US-10-238-965-4

Query Match          60.6%; Score 20; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FILE 4
      ||||
Db      1 FILE 4

Search completed: November 4, 2004, 01:43:17
Job time : 70.6667 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 4, 2004, 00:42:19 ; Search time 16.6667 Seconds
(without alignments)
27.854 Million cell updates/sec

Title: US-09-712-819D-12
Perfect score: 33
Sequence: 1 FTLEISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	33	100.0	100	4	US-09-840-459-32	Sequence 32, Appl
2	33	100.0	100	4	US-09-497-625A-32	Sequence 32, Appl
3	33	100.0	112	4	US-09-840-459-55	Sequence 55, Appl
4	33	100.0	112	4	US-09-497-625A-55	Sequence 55, Appl
5	33	100.0	113	2	US-08-672-345C-5	Sequence 5, Appl
6	33	100.0	113	2	US-08-672-345C-6	Sequence 6, Appl
7	33	100.0	113	2	US-08-672-345C-7	Sequence 7, Appl
8	33	100.0	113	2	US-08-672-345C-8	Sequence 8, Appl
9	33	100.0	113	2	US-08-672-345C-95	Sequence 95, Appl
10	33	100.0	113	2	US-08-672-345C-96	Sequence 96, Appl
11	33	100.0	113	2	US-08-672-345C-97	Sequence 97, Appl
12	33	100.0	113	2	US-08-672-345C-98	Sequence 98, Appl
13	33	100.0	113	3	US-09-214-095D-5	Sequence 5, Appl
14	33	100.0	113	3	US-09-214-095D-6	Sequence 6, Appl
15	33	100.0	113	3	US-09-214-095D-7	Sequence 7, Appl
16	33	100.0	113	3	US-09-214-095D-8	Sequence 8, Appl
17	33	100.0	113	3	US-09-214-095D-100	Sequence 100, App
18	33	100.0	113	3	US-09-214-095D-104	Sequence 104, App
19	33	100.0	113	3	US-09-214-095D-108	Sequence 108, App
20	33	100.0	113	3	US-09-214-095D-112	Sequence 112, App
21	33	100.0	280	4	US-09-214-095D-119	Sequence 119, App
22	33	100.0	348	4	US-09-646-028-12	Sequence 12, Appl
23	33	100.0	361	4	US-09-646-028-14	Sequence 14, Appl
24	30	90.9	192	4	US-09-328-352-5032	Sequence 5032, Ap
25	29	87.9	32	1	US-08-477-877B-33	Sequence 33, Appl
26	29	87.9	32	1	US-07-977-696C-71	Sequence 71, Appl
27	29	87.9	32	1	US-08-129-930B-71	Sequence 71, Appl

28	29	87.9	32	2	US-08-472-281A-33	Sequence 33, Appl
29	29	87.9	32	2	US-08-477-989B-33	Sequence 33, Appl
30	29	87.9	32	3	US-08-976-288A-71	Sequence 71, Appl
31	29	87.9	32	4	US-09-563-222C-80	Sequence 80, Appl
32	29	87.9	32	4	US-09-563-222C-114	Sequence 114, App
33	29	87.9	81	1	US-08-497-312-19	Sequence 19, Appl
34	29	87.9	81	4	US-09-254-180C-154	Sequence 154, App
35	29	87.9	81	4	US-09-254-180C-155	Sequence 155, App
36	29	87.9	81	4	US-09-254-180C-156	Sequence 156, App
37	29	87.9	81	4	US-09-254-180C-157	Sequence 157, App
38	29	87.9	81	4	US-09-254-180C-158	Sequence 158, App
39	29	87.9	81	4	US-09-254-180C-159	Sequence 159, App
40	29	87.9	100	4	US-09-472-087-113	Sequence 113, App
41	29	87.9	100	4	US-09-472-087-115	Sequence 115, App
42	29	87.9	100	4	US-09-840-459-21	Sequence 21, Appl
43	29	87.9	100	4	US-09-840-459-22	Sequence 22, Appl
44	29	87.9	100	4	US-09-840-459-23	Sequence 23, Appl
45	29	87.9	100	4	US-09-840-459-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-840-459-32
; Sequence 32, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-32

Query Match 100.0%; Score 33; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLEISR 7
|||
Db 76 FTLEISR 82

RESULT 2
US-09-497-625A-32
; Sequence 32, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran

```

; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-497-625A-32

Query Match      100.0%; Score 33; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLEISR 7
      |||||
Db      76 FTLEISR 82

RESULT 3
US-09-840-459-55
; Sequence 55, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-459-55

Query Match      100.0%; Score 33; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLEISR 7
      |||||
Db      76 FTLEISR 82

RESULT 4
US-09-497-625A-55
; Sequence 55, Application US/09497625A
; Patent No. 6727349
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; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-497-625A-55

Query Match      100.0%; Score 33; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLEISR 7
      |||||
Db      76 FTLEISR 82

RESULT 5
US-08-672-345C-5
; Sequence 5, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-345C-5
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Query Match 100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 6
US-08-672-345C-6
; Sequence 6, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-672-345C-6

Query Match 100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 7
US-08-672-345C-7
; Sequence 7, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

Query Match 100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 8
US-08-672-345C-8
; Sequence 8, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-672-345C-7

Query Match 100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 8
US-08-672-345C-8
; Sequence 8, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-672-345C-8

Query Match 100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 8
US-08-672-345C-8
; Sequence 8, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

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Query Match      100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	1	FTLEISR	7
D _b	76	FTLEISR	82

RESULT 9
US-08-672-345C-95
; Sequence 95, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-672-345C-95

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Query Match      100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	1	FTLEISR	7
Dp	76	FTLEISR	82

RESULT 10
US-08-672-345C-96
; Sequence 96, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA

; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/672,345C
 ; FILING DATE: 24-JUN-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 0575/51400
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-278-0400
 ; TELEFAX: 212-391-0525
 ; INFORMATION FOR SEQ ID NO: 96:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 113 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-672-345C-96

Query Match	100.0%;	Score 33;	DB 2;	Length 113;
Best Local Similarity	100.0%;	Pred. No. 4.4;		
Matches	7:	Conservative	0: Mismatches	0: Indels
			0: Gaps	0: Gaps

QY	1	FTLEISR	7
db	76	FTLEISR	82

RESULT 11
US-08-672-345C-97
; Sequence 97, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-672-345C-97

Query Match 100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 12

US-08-672-345C-98
; Sequence 98, Application US/08672345C
; Patent No. 5948658

; GENERAL INFORMATION:

; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/672,345C

; FILING DATE: 24-JUN-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/51400

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-278-0400

; TELEFAX: 212-391-0525

; INFORMATION FOR SEQ ID NO: 98:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 113 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-672-345C-98

Query Match 100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 13

US-09-214-095D-5
; Sequence 5, Application US/09214095D
; Patent No. 6280987

; GENERAL INFORMATION:

; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/214,095D

; CURRENT FILING DATE: 1999-07-19

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 5

; LENGTH: 113

; TYPE: PRT

; ORGANISM: Murinae gen. Sp.

US-09-214-095D-5

Query Match 100.0%; Score 33; DB 3; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 14

US-09-214-095D-6

; Sequence 6, Application US/09214095D

; Patent No. 6280987

; GENERAL INFORMATION:

; APPLICANT: Landry, Donald

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; FILE REFERENCE: 51400-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/214,095D

; CURRENT FILING DATE: 1999-07-19

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 6

; LENGTH: 113

; TYPE: PRT

; ORGANISM: Murinae gen. sp.

US-09-214-095D-6

Query Match

100.0%; Score 33; DB 3; Length 113;

Best Local Similarity 100.0%; Pred. No. 4.4;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7

Db 76 FTLEISR 82

RESULT 15

US-09-214-095D-7

; Sequence 7, Application US/09214095D

; Patent No. 6280987

; GENERAL INFORMATION:

; APPLICANT: Landry, Donald

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; FILE REFERENCE: 51400-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/214,095D

; CURRENT FILING DATE: 1999-07-19

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 7

; LENGTH: 113

; TYPE: PRT

; ORGANISM: Murinae gen. sp.

US-09-214-095D-7

Query Match

100.0%; Score 33; DB 3; Length 113;

Best Local Similarity 100.0%; Pred. No. 4.4;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7

Db 76 FTLEISR 82

Search completed: November 4, 2004, 00:54:52
Job time : 17.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 07:01:24 ; Search time 37 Seconds
(without alignments)
12.547 Million cell updates/sec

Title: US-09-712-819D-6
Perfect score: 33
Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 58200

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	20	60.6	7	1	US-08-222-619-8
2	20	60.6	7	5	PCT-US95-04075-8
3	19	57.6	6	6	5252328-8
4	18	54.5	7	1	US-08-346-333-24
5	18	54.5	7	3	US-09-268-992-78
6	18	54.5	7	3	US-09-657-474-78
7	18	54.5	7	4	US-08-753-750B-20
8	18	54.5	7	5	PCT-US91-07506-24
9	17	51.5	7	2	US-09-174-060-17
10	17	51.5	7	3	US-08-654-623-69
11	17	51.5	7	3	US-08-338-382-17
12	17	51.5	7	4	US-09-345-264-17
13	16	48.5	5	3	US-08-591-632-23
14	16	48.5	5	3	US-09-611-451-23
15	16	48.5	6	1	US-07-717-331F-5
16	16	48.5	6	4	US-08-757-425B-44
17	16	48.5	7	1	US-07-634-641-12
18	16	48.5	7	1	US-08-136-743B-55
19	16	48.5	7	3	US-09-040-216-28
20	16	48.5	7	3	US-09-173-941-72
21	16	48.5	7	4	US-09-423-468A-6
22	16	48.5	7	4	US-09-756-223A-26
23	16	48.5	7	4	US-09-494-190-72
24	15	45.5	4	1	US-08-305-871A-17
25	15	45.5	4	4	US-08-788-822A-1
26	15	45.5	4	4	US-08-134-231C-36
27	15	45.5	4	4	US-08-728-160-36

28	15	45.5	5	1	US-08-136-743B-63	Sequence 63, Appl
29	15	45.5	5	3	US-09-040-216-55	Sequence 55, Appl
30	15	45.5	5	3	US-08-591-632-17	Sequence 17, Appl
31	15	45.5	5	3	US-08-591-632-26	Sequence 26, Appl
32	15	45.5	5	3	US-09-611-451-17	Sequence 17, Appl
33	15	45.5	5	3	US-09-611-451-26	Sequence 26, Appl
34	15	45.5	6	1	US-08-136-743B-62	Sequence 62, Appl
35	15	45.5	6	1	US-08-357-264-6	Sequence 6, Appli
36	15	45.5	6	1	US-08-297-731-4	Sequence 4, Appli
37	15	45.5	6	1	US-08-222-619-21	Sequence 21, Appl
38	15	45.5	6	1	US-08-290-448A-41	Sequence 41, Appl
39	15	45.5	6	1	US-08-672-514-6	Sequence 6, Appli
40	15	45.5	6	1	US-08-290-448A-41	Sequence 41, Appl
41	15	45.5	6	1	US-08-175-069A-41	Sequence 41, Appl
42	15	45.5	6	2	US-08-637-759B-219	Sequence 219, App
43	15	45.5	6	3	US-08-871-355A-219	Sequence 219, App
44	15	45.5	6	3	US-09-040-216-54	Sequence 54, Appl
45	15	45.5	6	3	US-09-623-618B-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-222-619-8
; Sequence 8, Application US/08222619
; Patent No. 5652352
; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henri
; APPLICANT: Lyons, David
; APPLICANT: Wurfel, Mark
; APPLICANT: Wright, Samuel
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Center, Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,619
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-222-619-8

Query Match 60.6%; Score 20; DB 1; Length 7;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||:
Db 1 FTFEYSR 7

RESULT 2
PCT-US95-04075-8
; Sequence 8, Application PC/TUS9504075
; GENERAL INFORMATION:

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;
; APPLICANT: AMGEN INC.
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Angen Center, Patent Operations/ARC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04075
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; PCT-US95-04075-8
;
; Query Match 60.6%; Score 20; DB 5; Length 7;
; Best Local Similarity 57.1%; Pred. No. 3.8e+05;
; Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;
; QY 1 FTLKISR 7
; Db 1 FTFEYSR 7
;
; RESULT 3
; 5252328-8
; Patent No. 5252328
; APPLICANT: FAULDS, DARYL; VISHOOT, MIMI; BROOKS, EMILY
; TITLE OF INVENTION: MYCOPLASMA HYOPNEUMONIAE ANTIGEN AND USES
; THEREFORE
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/335,726
; FILING DATE: 07-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 30,130
; FILING DATE: 26-MAR-1987
; SEQ ID NO: 8:
; LENGTH: 6
; 5252328-8
;
; Query Match 57.6%; Score 19; DB 6; Length 6;
; Best Local Similarity 80.0%; Pred. No. 3.8e+05;
; Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 FTLKI 5
; Db 2 FVLKI 6
;
; RESULT 4
; US-08-346-333-24
; Sequence 24, Application US/08346333
; Patent No. 5677153
; GENERAL INFORMATION:
; APPLICANT: Botstein, David
; APPLICANT: Palzkill, Timothy
; TITLE OF INVENTION: Methods for modifying DNA and for
; TITLE OF INVENTION: detecting effects of such modification on interaction of
;
;
; TITLE OF INVENTION: encoded modified polypeptides with target substrates.
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard F. Trecartin
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,333
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/039,501
; FILING DATE:
; APPLICATION NUMBER: US 07/602,158
; FILING DATE: 22-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-53469/RPT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-346-333-24
;
; Query Match 54.5%; Score 18; DB 1; Length 7;
; Best Local Similarity 100.0%; Pred. No. 3.8e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 2 TLKI 5
; Db 2 TLKI 5
;
; RESULT 5
; US-09-268-992-78
; Sequence 78, Application US/09268992
; Patent No. 6342351
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; APPLICANT: Freimer, N.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/09/268,992
; CURRENT FILING DATE: 1999-03-16
; EARLIER APPLICATION NUMBER: 09/236,134
; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: 60/106,056
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 60/088,312
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/078,044
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
;

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; ORGANISM: Homo sapiens
US-09-268-992-78

Query Match 54.5%; Score 18; DB 3; Length 7;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKIS 6
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Db 2 YTMKYS 7

RESULT 6
US-09-657-474-78
; Sequence 78, Application US/09657474
; Patent No. 6399762
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; APPLICANT: Freimer, N.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/09/657,474
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 09/268,992
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/236,134
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/106,056
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/088,312
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/078,044
; PRIOR FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-657-474-78

Query Match 54.5%; Score 18; DB 3; Length 7;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKIS 6
:|:|
Db 2 YTMKYS 7

RESULT 7
US-08-753-750B-20
; Sequence 20, Application US/08753750B
; Patent No. 6610506
; GENERAL INFORMATION:
; APPLICANT: Lo, Reggie Y.C.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Potter, Andrew A.
; TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF
; TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME
; FILE REFERENCE: A34762 021645.0105
; CURRENT APPLICATION NUMBER: US/08/753,750B
; CURRENT FILING DATE: 1996-11-29
; PRIOR APPLICATION NUMBER: CA 2,164,274
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 60/008,569
; PRIOR FILING DATE: 1995-12-01
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 7
; TYPE: PRT

; ORGANISM: Escherichia coli
US-08-753-750B-20

Query Match 54.5%; Score 18; DB 4; Length 7;
Best Local Similarity 60.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKI 5
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Db 1 FTLSV 5

RESULT 8
PCT-US91-07506-24
; Sequence 24, Application PC/TUS9107506
; GENERAL INFORMATION:
; APPLICANT: Botstein, David
; APPLICANT: Palzkill, Timothy
; TITLE OF INVENTION: Methods for modifying DNA and for
; TITLE OF INVENTION: detecting effects of such modification on interaction of
; TITLE OF INVENTION: encoded modified polypeptides with target substrates.
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard F. Trecartin
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/07506
; FILING DATE: 19911021
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: FP-53469-PC/RFT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US91-07506-24

Query Match 54.5%; Score 18; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKI 5
:|:|
Db 2 TLKI 5

RESULT 9
US-09-174-060-17
; Sequence 17, Application US/09174060
; Patent No. 5989554
; GENERAL INFORMATION:
; APPLICANT: Knuth, Mark W
; APPLICANT: Haak-Frendscho, Mary
; APPLICANT: Shultz, John W
; APPLICANT: Lesley, Scott A
; APPLICANT: Villars, Catherine E

```
Query Match      51.5%; Score 17; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3: Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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RESULT 10
US-08-654-623-69
; Sequence 69, Application US/08654623
; Patent No. 6010884
; GENERAL INFORMATION:
; APPLICANT: Griffiths, Andrew D
; APPLICANT: Holliger, Kaspar-Philipp
; APPLICANT: Nissim, Ahuva
; APPLICANT: Fisch, Igor
; APPLICANT: Winter, Gregory P
; TITLE OF INVENTION: Recombinant Binding Proteins and Peptides
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/654,623

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Query Match          51.5%; Score 17; DB 3; Length 7;
Best Local Similarity 60.0%; Pred. No. 3.8e+05;
Matches             3: Conservative      2: Mismatches 0; Indels 0; Gaps 0;
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Qy 2 TLKIS 6
pb 1 SLKVS 5
:|:|

RESULT 11
US-08-338-382-17
; Sequence 17, Application US/08338382
; Patent No. 6069230
; GENERAL INFORMATION:
; APPLICANT: Knuth, Mark W
; APPLICANT: Haak-Frendscho, Mary
; APPLICANT: Shultz, John W
; APPLICANT: Lesley, Scott A
; APPLICANT: Villars, Catherine E
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION AND FACILE
; TITLE OF INVENTION: PURIFICATION OF PROTEINS, PEPTIDES AND CONJUGATES FOR
; TITLE OF INVENTION: IMMUNIZATION, PURIFICATION AND DETECTION APPLICATIONS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ross & Stevens, S.C.
; STREET: 1 South Pinckney St.
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701
; COMPUTER READABLE FORM:

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;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,382
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.024
; TELEPHONE: 608-257-5353
; TELEFAX: 608-257-9175
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-338-382-17

Query Match          51.5%; Score 17; DB 3; Length 7;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLK 4
Db 1 YTLK 4

RESULT 12
US-09-345-264-17
; Sequence 17, Application US/09345264
; Patent No. 6764689
; GENERAL INFORMATION:
; APPLICANT: Knuth, Mark W
; Haak-Frendscho, Mary
; Shultz, John W
; Lesley, Scott A
; Villars, Catherine E
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION AND FACILE
; PURIFICATION OF PROTEINS, PEPTIDES AND CONJUGATES FOR
; IMMUNIZATION, PURIFICATION AND DETECTION APPLICATIONS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ross & Stevens, S.C.
; STREET: 1 South Pinckney St.
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/345,264
; FILING DATE: 30-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/174,060
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-257-5353
; TELEFAX: 608-257-9175
;
```

```
;
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-345-264-17

Query Match          51.5%; Score 17; DB 4; Length 7;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLK 4
Db 1 YTLK 4

RESULT 13
US-08-591-632-23
; Sequence 23, Application US/08591632
; Patent No. 6261558
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Burton, Dennis R.
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,632
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/11907
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 26-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 19-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-591-632-23
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Query Match 48.5%; Score 16; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLK 4
Db 2 FTLQ 5

RESULT 14
US-09-611-451-23
; Sequence 23, Application US/09611451
; Patent No. 6395275
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; Burton, Dennis R.
; Lerner, Righard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; Patent Counsel
; STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/611,451
FILING DATE: 06-Jul-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/591,632
FILING DATE: 2001-10-29
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-611-451-23

Query Match 48.5%; Score 16; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLK 4
Db 2 FTLQ 5

RESULT 15
US-07-717-331F-5
; Sequence 5, Application US/07717331F

; Patent No. 5484905
; GENERAL INFORMATION:
; APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua
; APPLICANT: Stein
; TITLE OF INVENTION: A Receptor Protein Kinase Gene
; TITLE OF INVENTION: Encoded At The Self-Incompatibility Locus
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/717,331F
; FILING DATE: June 19th 1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-717-331F-5

Query Match 48.5%; Score 16; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LKIS 6
Db 2 LKVS 5

Search completed: November 4, 2004, 07:11:06
Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:36:19 ; Search time 19 Seconds
(without alignments)
35.448 Million cell updates/sec

Title: US-09-712-819D-12
Perfect score: 33
Sequence: 1 FTLEISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	33	100.0	74	2	G30538
2	33	100.0	112	1	KVMS16
3	33	100.0	113	1	KVMS51
4	33	100.0	120	1	KVMS67
5	33	100.0	127	2	S40323
6	33	100.0	133	2	S40324
7	29	87.9	54	2	S34093
8	29	87.9	56	2	I55399
9	29	87.9	71	2	H30538
10	29	87.9	72	2	S40358
11	29	87.9	75	2	S40337
12	29	87.9	83	2	S24211
13	29	87.9	83	2	S34095
14	29	87.9	87	2	S34091
15	29	87.9	87	2	S34094
16	29	87.9	89	2	B25155
17	29	87.9	91	2	S42186
18	29	87.9	91	2	S25463
19	29	87.9	93	2	PH1039
20	29	87.9	94	2	PL0258
21	29	87.9	96	2	S40320
22	29	87.9	99	2	E28833
23	29	87.9	99	2	S24504
24	29	87.9	99	2	S24501
25	29	87.9	100	2	S45440
26	29	87.9	100	2	S24681
27	29	87.9	100	2	S26334
28	29	87.9	101	2	C34153
29	29	87.9	101	2	A33730

30	29	87.9	101	2	PH1057	Ig light chain V r
31	29	87.9	102	2	S14590	Ig kappa chain V r
32	29	87.9	102	2	S14591	Ig kappa chain V r
33	29	87.9	102	2	S14594	Ig kappa chain V r
34	29	87.9	102	2	S14592	Ig kappa chain V r
35	29	87.9	102	2	S14593	Ig kappa chain V r
36	29	87.9	102	2	PH1035	Ig light chain V r
37	29	87.9	102	2	E28195	Ig kappa chain V r
38	29	87.9	102	2	PH1044	Ig light chain V r
39	29	87.9	103	2	PH1099	Ig light chain V r
40	29	87.9	103	2	PH1056	Ig light chain V r
41	29	87.9	103	2	PH1100	Ig light chain V r
42	29	87.9	103	2	PH1041	Ig light chain V r
43	29	87.9	103	2	PH1098	Ig light chain V r
44	29	87.9	103	2	PH1040	Ig light chain V r
45	29	87.9	103	2	PH1045	Ig light chain V r

ALIGNMENTS

RESULT 1

G30538
Ig kappa chain V region (253.15E2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996
C;Accession: G30538
R;Claflin, J.L.; Berry, J.
J. Immunol. 141, 4012-4019, 1988
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pne
A;Reference number: A30534; MUID:89035545; PMID:3141511
A;Accession: G30538
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr
A;Molecule type: mRNA
A;Residues: 1-74 <CLA>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7

Db 45 FTLEISR 51

RESULT 2

KVMS16
Ig kappa chain V region (M167) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004
C;Accession: A01908
R;Rudikoff, S.; Potter, M.
Biochemistry 17, 2703-2707, 1978
A;Title: kappa-Chain variable region from M167, a phosphorylcholine binding myeloma prot
A;Reference number: A01908; MUID:79000273; PMID:99160
A;Accession: A01908
A;Molecule type: protein
A;Residues: 1-112 <RUD>
A;Cross-references: UNIPROT:P01626
C;Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa
chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-95/Domain: immunoglobulin homology <IMM>
F;23-93/Disulfide bonds: #status predicted

Query Match 100.0%; Score 33; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
| | | | |
Db 76 FTLEISR 82

RESULT 3
KVMS51
Ig kappa chain V region (M511) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C:Accession: A01910
R:Appella, E.
Mol. Immunol. 17, 711-718, 1980
A:Title: Amino acid sequence of the light chain variable region of M511, a phosphorylated
A:Reference number: A01910; MUID:81052016; PMID:6776396
A:Accession: A01910
A:Molecule type: protein
A:Residues: 1-113 <APP>
A:Cross-references: UNIPROT:P01628
C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-95/Domain: immunoglobulin homology <IMM>
F:23-93/Disulfide bonds: #status predicted

Query Match 100.0%; Score 33; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
| | | | |
Db 76 FTLEISR 82

RESULT 4
KVMS67
Ig kappa chain precursor V region (VK167) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C:Accession: A01909
R:Selsing, E.; Storb, U.
Cell 25, 47-58, 1981
A:Title: Somatic mutation of immunoglobulin light-chain variable-region genes.
A:Reference number: A01909; MUID:82002223; PMID:6791832
A:Accession: A01909
A:Molecule type: DNA
A:Residues: 1-120 <SEL>
A:Cross-references: UNIPROT:P01627
A:Note: the sequence was determined from the germline gene
C:Genetics:
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-120/Product: Ig kappa chain V region (VK167) #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>
F:43-113/Disulfide bonds: #status predicted

Query Match 100.0%; Score 33; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
| | | | |
Db 96 FTLEISR 102

RESULT 5
S40323

Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40323
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40323
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-127 <KLE>
A:Cross-references: EMBL:X72433; NID:G441334; PIDN:CAA51101.1; PID:G441335
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:30-110/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
| | | | |
Db 91 FTLEISR 97

RESULT 6
S40324
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S40324
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40324
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-133 <KLE>
A:Cross-references: UNIPROT:Q8TCD0; EMBL:X72434
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-112/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
| | | | |
Db 93 FTLEISR 99

RESULT 7
S34093
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 07-May-1999
C:Accession: S34093
R:Wagner, S.D.; Iuzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34093
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-54 <WAG>
A:Cross-references: EMBL:X67177
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

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Query Match      87.9%; Score 29; DB 2; Length 54;
Best Local Similarity 85.7%; Pred. No. 4.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 43 FTLKISR 49

RESULT 8
I55399
SERCA3 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I55399
R;Wuytack, F.; Papp, B.; Verboomen, H.; Raeymaekers, L.; Dode, L.; Bobe, R.; Enouf, J.;
J. Biol. Chem. 269, 1410-1416, 1994
A;Title: A sarco/endoplasmic reticulum Ca(2+)-ATPase 3-type Ca2+ pump is expressed in pl
A;Reference number: I55399; MUID:94117459; PMID:8288608
A;Accession: I55399
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-56 <RES>
A;Cross-references: UNIPROT:Q93084; GB:S68239; NID:G544921; PIDN:AAB29700.1; PID:G544922
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C;Keywords: ATP

Query Match      87.9%; Score 29; DB 2; Length 56;
Best Local Similarity 85.7%; Pred. No. 4.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 30 FTLKISR 36

RESULT 9
H30538
Ig kappa chain V region (174.3F4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 09-May-1997
C:Accession: H30538
R;Clafin, J.L.; Berry, J.
J. Immunol. 141, 4012-4019, 1988
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneu
A;Reference number: A30534; MUID:89035545; PMID:3141511
A;Accession: H30538
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-71 <CLA>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match      87.9%; Score 29; DB 2; Length 71;
Best Local Similarity 85.7%; Pred. No. 6.3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 35 FTLKISR 41

RESULT 10
S40358
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C:Accession: S40358
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40358
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A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-72 <KLE>
A;Cross-references: EMBL:X72468; NID:G441404; PIDN:CAA51136.1; PID:G441405
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Query Match      87.9%; Score 29; DB 2; Length 72;
Best Local Similarity 85.7%; Pred. No. 6.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 FTLKISR 7
Db 28 FTLKISR 34
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RESULT 11
S40337
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C:Accession: S40337
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40337
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-75 <KLE>
A;Cross-references: EMBL:X72447; NID:G441362; PIDN:CAA51115.1; PID:G441363
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Query Match      87.9%; Score 29; DB 2; Length 75;
Best Local Similarity 85.7%; Pred. No. 6.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 FTLKISR 7
Db 30 FTLKISR 36
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RESULT 12
S24211
Ig kappa chain V region (V3a) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S24211
R;Pargent, W.; Meindl, A.; Thiebe, R.; Mitzel, S.; Zachau, H.G.
Eur. J. Immunol. 21, 1821-1827, 1991
A;Title: The human immunoglobulin kappa locus. Characterization of the duplicated O reg
A;Reference number: S24205; MUID:91330953; PMID:1907917
A;Accession: S24211
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-83 <PAR>
A;Cross-references: EMBL:X59317; NID:G33270; PIDN:CAA42004.1; PID:G33271
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Query Match      87.9%; Score 29; DB 2; Length 83;
Best Local Similarity 85.7%; Pred. No. 7.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 FTLKISR 7
Db 59 FTLKISR 65
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RESULT 13
S34095
Ig kappa chain V region - human
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C;Superfamily: immunoglobulin V region; immunoglobulin homology		C;Keywords: heterotetramer; immunoglobulin	
F;3-82/Domain: immunoglobulin homology <IMM>		Query Match 87.9%; Score 29; DB 2; Length 87;	
		Best Local Similarity 85.7%; Pred. No. 7.7;	
		Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 FTLEISR 7		
Db	63 FTLKISR 69		
Search completed: November 4, 2004, 00:48:41			
Job time : 20 secs			

C;Species: Homo sapiens (man)		C;Superfamily: immunoglobulin V region; immunoglobulin homology	
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004		C;Keywords: heterotetramer; immunoglobulin	
C;Accession: S34095		F;1-80/Domain: immunoglobulin homology <IMM>	
R;Wagner, S.D.; Luzzatto, L.		Query Match 87.9%; Score 29; DB 2; Length 83;	
Eur. J. Immunol. 23, 391-397, 1993		Best Local Similarity 85.7%; Pred. No. 7.4;	
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed		Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
A;Reference number: S34076; MUID:93170387; PMID:8436174			
A;Accession: S34095		QY 1 FTLEISR 7	
A;Status: preliminary		Db 61 FTLKISR 67	
A;Molecule type: DNA			
A;Residues: 1-83 <WAG>			
A;Cross-references: UNIPROT:Q8TCD0; UNIPROT:Q9UL80; EMBL:X67179			
C;Superfamily: immunoglobulin V region; immunoglobulin homology			
C;Keywords: heterotetramer; immunoglobulin			
F;1-80/Domain: immunoglobulin homology <IMM>			
Query Match 87.9%; Score 29; DB 2; Length 83;			
Best Local Similarity 85.7%; Pred. No. 7.4;			
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
QY	1 FTLEISR 7		
Db	61 FTLKISR 67		
RESULT 14			
S34091			
Ig kappa chain V region (patient 19 and 20) - human (fragment)			
C;Species: Homo sapiens (man)			
C;Date: 13-Jan-1995 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004			
C;Accession: S34091; S34092			
R;Wagner, S.D.; Luzzatto, L.			
Eur. J. Immunol. 23, 391-397, 1993			
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed			
A;Reference number: S34076; MUID:93170387; PMID:8436174			
A;Accession: S34091			
A;Molecule type: DNA			
A;Residues: 1-87 <WAG>			
A;Cross-references: UNIPROT:Q8NEK0; EMBL:X67175			
A;Experimental source: patient 19			
A;Accession: S34092			
A;Molecule type: DNA			
A;Residues: 1-87 <WAW>			
A;Cross-references: EMBL:X67176			
A;Experimental source: patient 20			
C;Superfamily: immunoglobulin V region; immunoglobulin homology			
C;Keywords: heterotetramer; immunoglobulin			
F;3-82/Domain: immunoglobulin homology <IMM>			
Query Match 87.9%; Score 29; DB 2; Length 87;		Query Match 87.9%; Score 29; DB 2; Length 87;	
Best Local Similarity 85.7%; Pred. No. 7.7;		Best Local Similarity 85.7%; Pred. No. 7.7;	
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 FTLEISR 7	QY	1 FTLEISR 7
Db	63 FTLKISR 69	Db	63 FTLKISR 69
RESULT 15			
S34094			
Ig kappa chain V region - human			
C;Species: Homo sapiens (man)			
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004			
C;Accession: S34094			
R;Wagner, S.D.; Luzzatto, L.			
Eur. J. Immunol. 23, 391-397, 1993			
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed			
A;Reference number: S34076; MUID:93170387; PMID:8436174			
A;Accession: S34094			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-87 <WAG>			
A;Cross-references: UNIPROT:Q9UL80; EMBL:X67178			

DT	21-JUL-1986 (Rel. 01, Created)	DR	EMBL; J00562; AAA39032.1; -.
DT	21-JUL-1986 (Rel. 01, Last sequence update)	DR	EMBL; K02415; AAA39051.1; -.
DT	05-JUL-2004 (Rel. 44, Last annotation update)	DR	PIR; A01909; KVM567.
DE	Ig kappa chain V-II region MOPC 511.	DR	HSSP; P01751; INQB.
OS	Mus musculus (Mouse).	DR	InterPro; IPR007110; Ig-like.
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	DR	InterPro; IPR003596; Ig_v.
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	DR	Pfam; PF00047; ig; 1.
OX	NCBI_TaxID=10090;	DR	SMART; SM00406; IGV; 1.
RN	[1]	DR	PROSITE; PS50835; IG_LIKE; 1.
RP	SEQUENCE.	KW	Immunoglobulin V region; Signal.
RX	MEDLINE=81052016; PubMed=6776396;	FT	SIGNAL 1 20
RA	Appella E.;	FT	CHAIN 21 120
RT	"Amino acid sequence of the light chain variable region of M511, a phosphorylcholine-binding murine myeloma protein.";	FT	DOMAIN 21 43
RL	Mol. Immunol. 17:711-718(1980).	FT	DOMAIN 44 59
CC	-!- MISCELLANEOUS: This chain was isolated from a myeloma protein that binds phosphorylcholine.	FT	DOMAIN 60 74
CC	PIR; A01910; KVM551.	FT	DOMAIN 75 81
DR	HSSP; Q8K0F8; 1KN2.	FT	DOMAIN 82 113
DR	InterPro; IPR007110; Ig-like.	FT	DOMAIN 114 120
DR	InterPro; IPR003596; Ig_v.	FT	DISULFID 43 113
DR	Pfam; PF00047; ig; 1.	SQ	SEQUENCE 120 AA; 13280 MW; 63BB571F0E4DE3E8 CRC64;
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS50835; IG_LIKE; 1.		
KW	Direct protein sequencing; Immunoglobulin V region.		
FT	DOMAIN 1 23		
FT	DOMAIN 24 39		
FT	DOMAIN 40 54		
FT	DOMAIN 55 61		
FT	DOMAIN 62 93		
FT	DOMAIN 94 102		
FT	DOMAIN 103 112		
FT	DISULFID 23 93		
FT	NON TER 113 113		
SQ	SEQUENCE 113 AA; 12496 MW; EFB0DC4DA2BD3450 CRC64;		
	Query Match 100.0%; Score 33; DB 1; Length 113;		
	Best Local Similarity 100.0%; Pred. No. 7.8;		
	Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 FTLEISR 7		
Db	76 FTLEISR 82		
	RESULT 3		
KV2B_MOUSE			
ID	KV2B_MOUSE STANDARD; PRT; 120 AA.		
AC	P01627;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Ig kappa chain V-II region VKappa167 precursor.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=82002223; PubMed=6791832;		
RA	Selsing E., Storb U.;		
RT	"Somatic mutation of immunoglobulin light-chain variable-region genes.";		
RL	Cell 25:47-58(1981).		
CC			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC			
	Query Match 90.9%; Score 30; DB 2; Length 306;		
	Best Local Similarity 85.7%; Pred. No. 1.2e+02;		
	Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
QY	1 FTLEISR 7		
Db	270 FTLEISR 276		
	RESULT 4		
Q87X30			
ID	Q87X30 PRELIMINARY; PRT; 306 AA.		
AC	Q87X30;		
DT	01-JUN-2003 (TrEMBLrel. 24, Created)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Dehydrogenase, putative.		
GN	OrderedLocusNames=PSPTO4360;		
OS	Pseudomonas syringae (pv. tomato).		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;		
OC	Pseudomonadaceae; Pseudomonas.		
OX	NCBI_TaxID=323;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=DC3000;		
RX	MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;		
RA	Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,		
RA	Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,		
RA	Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,		
RA	Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q.,		
RA	Khoury H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,		
RA	Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,		
RA	Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,		
RA	Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,		
RA	Bender C.L., White O., Fraser C.M., Collmer A.;		
RT	"The complete genome sequence of the Arabidopsis and tomato pathogen Pseudomonas syringae pv. tomato DC3000.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).		
DR	EMBL; AE016871; AAC57810.1; -.		
DR	TIGR; PSPTO4360; -.		
KW	Complete proteome.		
SQ	SEQUENCE 306 AA; 34515 MW; D13FCA5790ACB33D CRC64;		

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RESULT 5
Q88PD2
ID Q88PD2 PRELIMINARY; PRT; 330 AA.
AC Q88PD2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 3-beta hydroxysteroid dehydrogenase/isomerase family protein,
DE putative.
DE OrderedLocusNames=PP0918;
GN Pseudomonas putida (strain KT2440).
OS Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapfle E.K., Scanlan D., Tran K.,
RA Moazzez A., Uterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808 (2002).
DR EMBL; AE016777; AAN66543.1; -.
DR TIGR; PP0918; -.
DR GO; GO:0016853; F:isomerase activity; IEA.
KW Complete proteome; Isomerase.
SQ SEQUENCE 330 AA; 37056 MW; A60498E263D91AC5 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 330;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 294 FTLEISR 300

RESULT 6
Q9HE63
ID Q9HE63 PRELIMINARY; PRT; 355 AA.
AC Q9HE63;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Related to cyclin homolog UME3.
GN Name=B2108.140;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the EMBL/GenBank/DBJ family.
DR EMBL; AL451012; CAC18151.1; -.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin_like.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; Cyclin_N; 1.
DR SMART; SM00385; CYCLIN; 1.
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KW Cyclin.
SQ SEQUENCE 355 AA; 39661 MW; A081A8CC97B9B00E CRC64;

Query Match 90.9%; Score 30; DB 2; Length 355;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 61 FTLEISR 67

RESULT 7
Q847Y6
ID Q847Y6 PRELIMINARY; PRT; 375 AA.
AC Q847Y6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gyrase B subunit (Fragment).
GN Name=gyrB;
OS Bacillus pumilus (Bacillus mesentericus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1408;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FO-036b;
RA Chen F., Venkateswaran K.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: DNA gyrase negatively supercoils closed circular double-
CC stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AY167867; AAO61450.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR001241; DNA_topoisom.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR PRINTS; PR00418; TFI2FAMILY.
DR SMART; SM00433; TOP2C; 1.
DR PROSITE; PS00177; TOPOISOMERASE II; 1.
KW ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1
FT NON_TER 375
SQ SEQUENCE 375 AA; 41568 MW; 04A49AD8704E3A6D CRC64;

Query Match 90.9%; Score 30; DB 2; Length 375;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 364 FTLEISR 370

RESULT 8
Q7Z3Y5
ID Q7Z3Y5 PRELIMINARY; PRT; 86 AA.
AC Q7Z3Y5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Rearranged VKA17 V gene segment (Fragment).
GN Name=VKA17;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```

```
[1]
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206024; AAF69322.1; -.
DR PIR; PL0258; PL0258.
DR PIR; S26334; S26334.
DR PDB; 1DLF; X-ray; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 86
FT SEQUENCE 86 AA; 9764 MW; D198FC04FE0C78FD CRC64;

Query Match 87.9%; Score 29; DB 2; Length 86;
Best Local Similarity 85.7%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 55 FTLKISR 61

RESULT 9
AAR11040 PRELIMINARY; PRT; 102 AA.
AC AAR11040;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.Sle1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.Sle1 mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436880; AAR11040.1; -.
FT NON_TER 1
FT NON_TER 102
FT SEQUENCE 102 AA; 11112 MW; A08600D2B09ABA92 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 102;
Best Local Similarity 85.7%; Pred. No. 68;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 74 FTLKISR 80

RESULT 10
Q9JL82 PRELIMINARY; PRT; 104 AA.
AC Q9JL82;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
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RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206024; AAF69322.1; -.
DR PIR; PL0258; PL0258.
DR PIR; S26334; S26334.
DR PDB; 1DLF; X-ray; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 104
FT SEQUENCE 104 AA; 11360 MW; 5DA8BFFD5F0AA1AE CRC64;

Query Match 87.9%; Score 29; DB 2; Length 104;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 68 FTLKISR 74

RESULT 11
AAR11024 PRELIMINARY; PRT; 104 AA.
AC AAR11024;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.Sle1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.Sle1 mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436864; AAR11024.1; -.
FT NON_TER 1
FT NON_TER 104
FT SEQUENCE 104 AA; 11310 MW; 2CF631F3058E2BB9 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 104;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 73 FTLKISR 79

RESULT 12
AAR11056 PRELIMINARY; PRT; 104 AA.
AC AAR11056;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN=B6.Sle1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.Sle1 mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436896; AAR11056.1; -.
FT NON_TER 1
FT NON_TER 104
SQ SEQUENCE 104 AA; 11327 MW; BFC116BEF36AB51A CRC64;

Query Match      87.9%; Score 29; DB 2; Length 104;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 73 FTLKISR 79

RESULT 13
AAR11063
ID AAR11063 PRELIMINARY; PRT; 104 AA.
AC AAR11063;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.Sle1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.Sle1 mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436903; AAR11063.1; -.
FT NON_TER 1
FT NON_TER 104
SQ SEQUENCE 104 AA; 11304 MW; 9358D08600C6E65A CRC64;

Query Match      87.9%; Score 29; DB 2; Length 104;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 74 FTLKISR 80

RESULT 14
AAR11074
ID AAR11074 PRELIMINARY; PRT; 105 AA.
AC AAR11074;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.Sle1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.Sle1 mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436914; AAR11074.1; -.
FT NON_TER 1
FT NON_TER 105
SQ SEQUENCE 105 AA; 11378 MW; BCB358D08600CEC0 CRC64;
```

```
Query Match      87.9%; Score 29; DB 2; Length 105;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 74 FTLKISR 80
```

```
RESULT 15
AAR10990
ID AAR10990 PRELIMINARY; PRT; 109 AA.
AC AAR10990;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.Sle1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.Sle1 mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436830; AAR10990.1; -.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11894 MW; BFA0941FA01908FD CRC64;
```

```
Query Match      87.9%; Score 29; DB 2; Length 109;
Best Local Similarity 85.7%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 68 FTLKISR 74
```

Search completed: November 4, 2004, 00:53:57
Job time : 105 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:33:03 ; Search time 60 Seconds
(without alignments)
41.852 Million cell updates/sec

Title: US-09-712-819D-12
Perfect score: 33
Sequence: 1 FTLEISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	33	100.0	32	7	ADM08848 Canine im
2	33	100.0	32	7	ADM08851 Canine im
3	33	100.0	32	7	ADM08547 Canine im
4	33	100.0	32	7	ADM08548 Canine im
5	33	100.0	100	4	Aae06969 Mouse ger
6	33	100.0	104	2	Aar40214 Sequence
7	33	100.0	111	5	Abg76560 HCV El an
8	33	100.0	112	4	Aae06992 Human kap
9	33	100.0	113	2	Aaw39803 Variable
10	33	100.0	113	2	Aaw39886 Light cha
11	33	100.0	113	2	Aaw39802 Variable
12	33	100.0	113	2	Aaw39801 Variable
13	33	100.0	113	2	Aaw39882 Variable
14	33	100.0	113	2	Aaw39804 Variable
15	33	100.0	113	8	ADI22125 Anti-plat
16	33	100.0	121	2	AAR47511 LS2H241 l
17	33	100.0	122	3	AAY70790 Murine an
18	33	100.0	145	3	AAY32261 Mouse ant
19	33	100.0	178	5	ABP43484 Human sec
20	33	100.0	248	7	ADG32323 Mouse scf
21	33	100.0	274	2	AAW39899 Single ch
22	33	100.0	317	7	ADG32360 Precursor
23	33	100.0	348	2	AAy29910 Human IP-
24	33	100.0	361	2	AAy29912 Human MCP
25	31	93.9	715	8	ADN38471 Novel hum

26	30	90.9	192	6	ADA33745	Ada33745 Acinetoba
27	30	90.9	330	6	ABU39673	Abu39673 Protein e
28	30	90.9	330	6	ABU41467	Abu41467 Protein e
29	30	90.9	335	6	ABU27800	Abu27800 Protein e
30	29	87.9	32	2	AAW79207	Aaw79207 Framework
31	29	87.9	32	4	AAB86295	Aab86295 Murine de
32	29	87.9	32	5	ABP62672	Abp62672 Human imm
33	29	87.9	32	5	ABP62674	Abp62674 Human imm
34	29	87.9	32	5	AAU70400	Aau70400 Mouse lig
35	29	87.9	32	5	AAU70440	Aau70440 Mouse lig
36	29	87.9	32	7	ADM08541	Adm08541 Canine im
37	29	87.9	32	7	ADM08539	Adm08539 Canine im
38	29	87.9	32	8	ADL93640	Adl93640 Human CD4
39	29	87.9	32	8	ADL93554	Adl93554 Human CD4
40	29	87.9	37	8	ADQ31286	Adq31286 Humanised
41	29	87.9	50	5	ABG30477	Abg30477 Human ant
42	29	87.9	50	5	ABG30478	Abg30478 Human ant
43	29	87.9	50	5	ABG30479	Abg30479 Human ant
44	29	87.9	81	2	AAR92994	Aar92994 Homologou
45	29	87.9	89	2	AAR80082	Aar80082 Mouse der

ALIGNMENTS

RESULT 1

ADM08848
ID ADM08848 standard; peptide; 32 AA.
XX
AC ADM08848;
XX
DT 20-MAY-2004 (first entry)
XX
DE Canine immunoglobulin kappa VL species framework 3 peptide 60.
XX
KW canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
KW antiallergic; allergy; IgE; gene therapy; kappa species; VL framework;
KW FR3.
XX
OS Canis familiaris.
XX
PN WO2003060080-A2.
XX
PD 24-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-US041362.
XX
PR 21-DEC-2001; 2001US-0344874P.
XX
PA (IDEX-) IDEXX LAB INC.
XX
PI Krah ER, Guo H, Aiyappa A, Lawton R;
XX
DR WPI; 2003-598521/56.
XX
PT New canine heavy and light chain variable domain polypeptides, useful for
PT treating canine allergy.
XX
PS Claim 43; Page 111; 130pp; English.
XX
CC The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates
CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (FR) peptide of the
CC invention.
XX
SQ Sequence 32 AA;

Query Match 100.0%; Score 33; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
| | | | |
Db 15 FTLEISR 21

RESULT 2
ADM08851
ID ADM08851 standard; peptide; 32 AA.

XX AC ADM08851;

XX DT 20-MAY-2004 (first entry)

XX DE Canine immunoglobulin kappa VL species framework 3 peptide 63.

XX KW canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
XX KW antiallergic; allergy; IgE; gene therapy; kappa species; VL framework;
XX KW FR3.

XX OS Canis familiaris.

XX PN WO2003060080-A2.

XX PD 24-JUL-2003.

XX PF 20-DEC-2002; 2002WO-US041362.

XX PR 21-DEC-2001; 2001US-0344874P.

XX PA (IDEX-) IDEXX LAB INC.

XX PI Krah ER, Guo H, Aiyappa A, Lawton R;

XX DR WPI; 2003-598521/56.

XX PT New canine heavy and light chain variable domain polypeptides, useful for
XX PT treating canine allergy.

XX PS Claim 43; Page 111; 130pp; English.

XX CC The invention relates to a novel canine heavy or light chain variable
XX CC domain polypeptide. The protein of the invention demonstrates
XX CC antiallergic activity and may be useful for treating canine allergy,
XX CC possibly via gene therapy. The current sequence is that of a canine
XX CC immunoglobulin light chain variable domain framework (FR) peptide of the
XX CC invention.

XX SQ Sequence 32 AA;

Query Match 100.0%; Score 33; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
| | | | |
Db 15 FTLEISR 21

RESULT 3
ADM08547
ID ADM08547 standard; peptide; 32 AA.

XX AC ADM08547;

XX DT 20-MAY-2004 (first entry)

XX DE Canine immunoglobulin kappa VL subgenus framework 3 peptide 24.

XX KW canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
XX KW antiallergic; allergy; IgE; gene therapy; kappa subgenus; VL framework;
XX KW FR3.

XX OS Canis familiaris.

XX PN WO2003060080-A2.
XX PD 24-JUL-2003.
XX PF 20-DEC-2002; 2002WO-US041362.
XX PR 21-DEC-2001; 2001US-0344874P.
XX PA (IDEX-) IDEXX LAB INC.
XX PI Krah ER, Guo H, Aiyappa A, Lawton R;
XX DR WPI; 2003-598521/56.
XX PT New canine heavy and light chain variable domain polypeptides, useful for
XX PT treating canine allergy.
XX PS Claim 42; Page 109; 130pp; English.
XX CC The invention relates to a novel canine heavy or light chain variable
XX CC domain polypeptide. The protein of the invention demonstrates
XX CC antiallergic activity and may be useful for treating canine allergy,
XX CC possibly via gene therapy. The current sequence is that of a canine
XX CC immunoglobulin light chain variable domain framework (FR) peptide of the
XX CC invention.
XX SQ Sequence 32 AA;

Query Match 100.0%; Score 33; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
| | | | |
Db 15 FTLEISR 21

RESULT 4
ADM08548
ID ADM08548 standard; peptide; 32 AA.

XX AC ADM08548;

XX DT 20-MAY-2004 (first entry)

XX DE Canine immunoglobulin kappa VL subgenus framework 3 peptide 25.

XX KW canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
XX KW antiallergic; allergy; IgE; gene therapy; kappa subgenus; VL framework;
XX KW FR3.

XX OS Canis familiaris.

XX PN WO2003060080-A2.

XX PD 24-JUL-2003.

XX PF 20-DEC-2002; 2002WO-US041362.

XX PR 21-DEC-2001; 2001US-0344874P.

XX PA (IDEX-) IDEXX LAB INC.

XX PI Krah ER, Guo H, Aiyappa A, Lawton R;

XX DR WPI; 2003-598521/56.

XX PT New canine heavy and light chain variable domain polypeptides, useful for
XX PT treating canine allergy.

XX PS Claim 42; Page 109; 130pp; English.

Thu Nov 4 07:26:50 2004

CC The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates
CC anti-allergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (FR) peptide of the
CC invention.
XX
SQ Sequence 32 AA;

Query Match 100.0%; Score 33; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 15 FTLEISR 21
|||||
15 FTLEISR 21

RESULT 5
AAE06969
ID AAE06969 standard; protein; 100 AA.
XX
AC AAE06969;
XX
DT 16-OCT-2001 (first entry)
XX
DE Mouse germline kappa light chain variable (VK) region, 167/24.
XX
KW Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
KW neuroprotective; immunosuppressive; human immunodeficiency virus;
KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;
KW inflammatory glomerulopathy; vascular intervention;
KW neointimal hyperplasia; VK; kappa light chain variable region.
XX
OS Mus sp.
XX
PN WO200157226-A1.
XX
PD 09-AUG-2001.
XX
PF 02-FEB-2001; 2001WO-US003537.
XX
PR 03-FEB-2000; 2000US-00497625.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
XX WPI; 2001-488888/53.
DR
XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated
XX disorder in a patient, comprises a binding specificity for CCR2, and a
XX non-human antigen binding region and human immunoglobulin.
XX
PS Disclosure; Page 151; 183pp; English.
XX
CC The patent discloses a humanised antibody or its antigen-binding
CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),
CC comprising an antigen binding region of non-human origin and at least a
CC portion of an immunoglobulin of human origin. The humanised antibodies
CC are useful for inhibiting the interaction of a cell expressing CCR2. They
CC are useful for inhibiting or treating HIV infection. The proteins of the
CC invention are useful for inhibiting leukocyte trafficking, for treating
CC CCR2-mediated disorders such as inflammatory disorder, autoimmune
CC disorders such as rheumatoid arthritis and multiple sclerosis,
CC atherogenesis and atherosclerosis, and for inhibiting restenosis. They
CC are useful in therapy or diagnosis, and in the manufacture of a
CC medicament for treating CCR-2 mediated disease. They are also useful for
CC treating allergy, anaphylaxis, malignancy, chronic and acute

CC inflammation, histamine and IGE-mediated allergic reaction, shock,
CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory
CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis
CC associated with vascular intervention, including angioplasty and/or stent
CC placement in a mammal. Humanised antibodies are also useful for
CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting
CC neointimal hyperplasia of a vessel in a mammal, preferably associated
CC with vascular intervention. The present sequence is mouse germline kappa
CC light chain variable (VK) region, 167/24
XX
SQ Sequence 100 AA;

Query Match 100.0%; Score 33; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82
|||||
76 FTLEISR 82

RESULT 6
AAR40214
ID AAR40214 standard; protein; 104 AA.
XX
AC AAR40214;
XX
DT 25-MAR-2003 (revised)
DT 04-FEB-1994 (first entry)
XX
DE Sequence of mouse hybridoma cell line RF-HBs-1 antibody light chain.
XX
KW Humanised antibody; complementarity determining region;
KW hepatitis B virus; surface antigen.
XX
OS Synthetic.
XX
PN WO9316192-A1.
XX
PD 19-AUG-1993.
XX
PF 09-FEB-1993; 93WO-GB000267.
XX
PR 11-FEB-1992; 92GB-00002796.
XX
PA (WELL) WELLCOME FOUND LTD.
XX
PI Crowe JS;
XX
DR WPI; 1993-272894/34.
DR N-PSDB; AAQ48172.
XX
PT Humanised antibody against hepatitis - has complementarity determining
PT regions of variable domains from a non-human antibody and constant
PT domains from a human antibody.
PS Disclosure; Page 24-25; 48pp; English.
XX
CC A humanised antibody is claimed in which the AA sequences of the CDRs are
CC at least 60% homologous with light chain CDRs 1-3, and heavy chain CDRs 1
CC -3 (see AAQ48174-9, AAR40216-21). The first step to humanise a monoclonal
CC antibody by CDR-grafting is to determine the nucleotide and predicted AA
CC sequence of the starting antibody light and heavy variable domains. The
CC simplest method is from CDNA. RF-HBs-1 is an hybridoma cell line. Its
CC Mabs contain mouse anti-hepatitis B surface antigen heavy and light
CC chains. The nucleotide and predicted AA sequence of the mouse RF-HBs-1
CC antibody chains are shown in AAQ48172/R40214 (light) and AAQ48173/R40215
CC (heavy). (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 104 AA;

Query Match 100.0%; Score 33; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 14;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
|||||
76 FTLEISR 82

Db

RESULT 7
ABG76560
ID ABG76560 standard; protein; 111 AA.
XX
AC ABG76560;
XX
DT 05-NOV-2002 (first entry)
XX
DE HCV E1 antigen monoclonal antibody #48.
XX
KW Human; HCV; hepatitis C virus; E1 antigen; monoclonal antibody; vaccine;
KW hepatotropic; Fab; hypervariable region; E2 antigen; antibody.
XX
OS Homo sapiens.
OS
FN WO200260954-A1.
XX
PD 08-AUG-2002.
XX
PF 14-JAN-2002; 2002WO-SE000044.
XX
PR 12-JAN-2001; 2001US-0260889P.
XX
PA (KARO-) KAROLINSKA INNOVATIONS AB.
XX
PI Drakenberg K, Persson MAA;
XX
DR WPI; 2002-608502/65.
XX
XX
PT Vaccine comprising a human monoclonal antibody against hepatitis C virus
PT (HCV) E1 or E2 antigen, useful for treating or preventing HCV infection.
XX
PS Disclosure; Page 53; 64pp; English.
XX
CC The invention relates to a human monoclonal antibody or its antigen
CC binding fragments, which exhibit immunological binding affinity for a
CC hepatitis C virus (HCV) E1 antigen, comprising an amino acid sequence
CC homologous to the binding portion of a human antibody Fab molecule from a
CC combinatorial antibody library. The vaccine composition comprising the
CC antibodies or antigen binding fragments against HCV E1 or E2 antigen or
CC its hypervariable region is useful in treating or preventing HCV
CC infection in a subject. Sequences ABG76513-ABG76568 represent human
CC monoclonal antibodies against HCV E1 antigen
XX
SQ Sequence 111 AA;

Query Match 100.0%; Score 33; DB 5; Length 111;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
|||||
75 FTLEISR 81

Db

RESULT 8
AAE06992
ID AAE06992 standard; protein; 112 AA.
XX
AC AAE06992;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human kappa light chain variable (VK) region, H66.
XX
KW Human; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;

KW neuroprotective; immunosuppressive; human immunodeficiency virus;
KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
KW multiple sclerosis; atherogenesis; atherosclerosis; stenosis; asthma;
KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;
KW inflammatory glomerulopathy; vascular intervention; 1D9 antibody;
KW neointimal hyperplasia; VK; kappa light chain variable region.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 24. .39
FT /label= CDR1
FT /note= "Complementarity determining region 1"
FT Region 55. .61
FT /label= CDR2
FT /note= "Complementarity determining region 2"
FT Region 94. .102
FT /label= CDR3
FT /note= "Complementarity determining region 3"
XX
PN WO200157226-A1.
XX
PD 09-AUG-2001.
XX
PF 02-FEB-2001; 2001WO-US003537.
XX
PR 03-FEB-2000; 2000US-00497625.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;
XX WPI; 2001-488888/53.
XX
PT Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated
PT disorder in a patient, comprises a binding specificity for CCR2, and a
PT non-human antigen binding region and human immunoglobulin.
XX
PS Disclosure; Page 159-160; 183pp; English.
XX
CC The patent discloses a humanised antibody or its antigen-binding
CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),
CC comprising an antigen binding region of non-human origin and at least a
CC portion of an immunoglobulin of human origin. The humanised antibodies
CC are useful for inhibiting the interaction of a cell expressing CCR2. They
CC are useful for inhibiting or treating HIV infection. The proteins of the
CC invention are useful for inhibiting leukocyte trafficking, for treating
CC CCR2-mediated disorders such as inflammatory disorder, autoimmune
CC disorders such as rheumatoid arthritis and multiple sclerosis,
CC atherogenesis and atherosclerosis, and for inhibiting restenosis. They
CC are useful in therapy or diagnosis, and in the manufacture of a
CC medicament for treating CCR-2 mediated disease. They are also useful for
CC treating allergy, anaphylaxis, malignancy, chronic and acute
CC inflammation, histamine and IGE-mediated allergic reaction, shock,
CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory
CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis
CC associated with vascular intervention, including angioplasty and/or stent
CC placement in a mammal. Humanised antibodies are also useful for
CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting
CC neointimal hyperplasia of a vessel in a mammal, preferably associated
CC with vascular intervention. The present sequence is human kappa light
CC chain variable (VK) region, H66
XX
SQ Sequence 112 AA;

Query Match 100.0%; Score 33; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
|||||

```
Db          76 FTLEISR 82

RESULT 9
AAW39803
ID AAW39803 standard; protein; 113 AA.
XX
AC AAW39803;
XX
DT 16-JUN-1998 (first entry)
XX
DE Variable domain of the Kappa light chain of catalytic antibody 12H1.
XX
KW Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction.
XX
OS Mus sp.
XX
PN WO9749800-A1.
XX
DT 31-DEC-1997.
XX
DE Variable domain of the Kappa light chain of catalytic antibody 12H1.
XX
KW Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction.
XX
OS Mus sp.
XX
PN WO9749800-A1.
XX
PD 31-DEC-1997.
XX
PF 25-JUN-1997; 97WO-US010965.
XX
PR 25-JUN-1996; 96US-00672345.
XX
PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI Landry DW;
XX
DR WPI; 1998-077166/07.
XX
DR N-PSDB; AAV09793.
XX
PT New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required in far
PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX
PS Disclosure; Fig 19; 147pp; English.
XX
CC The present sequence represents the light chain of a catalytic antibody
CC which is capable of degrading cocaine. A series of cocaine transition
CC state analogues (TSAs) were prepared and used to immunise mice for
CC production of hybridomas. Catalytic antibodies were identified by their
CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The
CC antibodies reduce the concentration of cocaine in a subject, and are used
CC particularly for the treatment of an overdose. They are also used for
CC treating addiction (by reducing the in vivo concentration that can be
CC achieved)
XX
SQ Sequence 113 AA;

Query Match          100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 11
AAW39802
ID AAW39802 standard; protein; 113 AA.
XX
AC AAW39802;
XX
DT 16-JUN-1998 (first entry)
XX
DE Variable domain of the Kappa light chain of catalytic antibody 6A12.
XX
KW Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction.
XX
OS Mus sp.
XX
PN WO9749800-A1.
XX
PD 31-DEC-1997.
XX
PF 25-JUN-1997; 97WO-US010965.
XX
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Db          76 FTLEISR 82

RESULT 10
AAW39886
ID AAW39886 standard; protein; 113 AA.
XX
AC AAW39886;
XX
DT 18-JUN-1998 (first entry)
XX
DE Light chain of the catalytic antibody 6A12.

Query Match          100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 10
AAW39886
ID AAW39886 standard; protein; 113 AA.
XX
AC AAW39886;
XX
DT 18-JUN-1998 (first entry)
XX
DE Light chain of the catalytic antibody 6A12.
```

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Db          76 FTLEISR 82

RESULT 9
AAW39803
ID AAW39803 standard; protein; 113 AA.
XX
AC AAW39803;
XX
DT 16-JUN-1998 (first entry)
XX
DE Variable domain of the Kappa light chain of catalytic antibody 12H1.
XX
KW Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction.
XX
OS Mus sp.
XX
PN WO9749800-A1.
XX
PD 31-DEC-1997.
XX
PF 25-JUN-1997; 97WO-US010965.
XX
PR 25-JUN-1996; 96US-00672345.
XX
PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI Landry DW;
XX
DR WPI; 1998-077166/07.
XX
DR P-PSDB; AAV09802.
XX
PT New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required in far
PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX
PS Claim 18; Page 73; 147pp; English.
XX
CC AAW39801-05 represent the amino acid sequences of the variable domain of
CC the Kappa light chain of catalytic antibodies which are able to degrade
CC cocaine. A series of cocaine transition state analogues (TSAs) were
CC prepared and used to immunise mice for production of hybridomas.
CC Catalytic antibodies were identified by their capacity to release 3H-
CC benzoic acid from 3H-phenyl cocaine. The 12H1 antibody (AAW39808
CC represents the heavy chain) was identified using TSA2, and has a per
CC minute Kcat of 0.016. The antibodies reduce the concentration of cocaine
CC in a subject, and are used particularly for the treatment of an overdose.
CC They are also used for treating addiction (by reducing the in vivo
CC concentration that can be achieved)
XX
SQ Sequence 113 AA;

Query Match          100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 10
AAW39886
ID AAW39886 standard; protein; 113 AA.
XX
AC AAW39886;
XX
DT 18-JUN-1998 (first entry)
XX
DE Light chain of the catalytic antibody 6A12.
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PR 25-JUN-1996; 96US-00672345.
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX Landry DW;
XX WPI; 1998-077166/07.
XX New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required in far
PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX
PS Claim 14; Page 72; 147pp; English.
XX
CC AAW39801-05 represent the amino acid sequences of the variable domain of
CC the Kappa light chain of catalytic antibodies which are able to degrade
CC cocaine. A series of cocaine transition state analogues (TSAs) were
CC prepared and used to immunise mice for production of hybridomas.
CC Catalytic antibodies were identified by their capacity to release 3H-
CC benzoic acid from 3H-phenyl cocaine. The 6A12 antibody (AAW39807
CC represents the heavy chain) was identified using TSA1, which is an
CC immunogenic conjugate of a phosphate monoester transition state analogue.
CC Antibody 6A12 has a per minute Kcat of 0.072. The antibodies reduce the
CC concentration of cocaine in a subject, and are used particularly for the
CC treatment of an overdose. They are also used for treating addiction (by
CC reducing the in vivo concentration that can be achieved)
XX
SQ Sequence 113 AA;
Query Match 100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLEISR 7
Db 76 FTLEISR 82
RESULT 12
AAW39801
ID AAW39801 standard; protein; 113 AA.
XX
AC AAW39801;
XX
XX 16-JUN-1998 (first entry)
DT
XX
DE Variable domain of the Kappa light chain of catalytic antibody 3B9.
XX
KW Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction.
XX
OS Mus sp.
XX
XX WO9749800-A1.
XX
XX 31-DEC-1997.
XX
XX 25-JUN-1997; 97WO-US010965.
XX
XX 25-JUN-1996; 96US-00672345.
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Landry DW;
XX
XX WPI; 1998-077166/07.
XX P-PSDB; AAV09791.
XX
XX New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required in far
PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX Claim 12; Page 71-72; 147pp; English.
XX
CC AAW39801-05 represent the amino acid sequences of the variable domain of
CC the Kappa light chain of catalytic antibodies which are able to degrade
CC cocaine. A series of cocaine transition state analogues (TSAs) were
CC prepared and used to immunise mice for production of hybridomas.
CC Catalytic antibodies were identified by their capacity to release 3H-
CC benzoic acid from 3H-phenyl cocaine. The 3B9 antibody (AAW39806
CC represents the heavy chain) was identified using TSA1, which is an
CC immunogenic conjugate of a phosphate monoester transition state analogue.
CC Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the
CC concentration of cocaine in a subject, and are used particularly for the
CC treatment of an overdose. They are also used for treating addiction (by
CC reducing the in vivo concentration that can be achieved)
XX
SQ Sequence 113 AA;
Query Match 100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLEISR 7
Db 76 FTLEISR 82
RESULT 13
AAW39882
ID AAW39882 standard; protein; 113 AA.
XX
AC AAW39882;
XX
XX 16-JUN-1998 (first entry)
DT
XX
DE Light chain of the catalytic antibody 2A10.
XX
KW Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction.
XX
OS Mus sp.
XX
XX WO9749800-A1.
XX
XX 31-DEC-1997.
XX
XX 25-JUN-1997; 97WO-US010965.
XX
XX 25-JUN-1996; 96US-00672345.
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Landry DW;
XX
XX WPI; 1998-077166/07.
XX N-PSDB; AAV09789.
XX
XX New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required in far
PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX
XX Disclosure; Fig 21; 147pp; English.
XX
CC The present sequence represents the light chain of a catalytic antibody
CC which is capable of degrading cocaine. A series of cocaine transition
CC state analogues (TSAs) were prepared and used to immunise mice for
CC production of hybridomas. Catalytic antibodies were identified by their
CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The
CC antibodies reduce the concentration of cocaine in a subject, and are used
CC particularly for the treatment of an overdose. They are also used for
CC treating addiction (by reducing the in vivo concentration that can be

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CC achieved)
XX
SQ Sequence 113 AA;

Query Match      100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 14
AAW39804
ID AAW39804 standard; protein; 113 AA.
XX
AC AAW39804;
XX
DT 16-JUN-1998 (first entry)
XX
DE Variable domain of the Kappa light chain of catalytic antibody 2A10.
XX
KW Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction.
XX
OS Mus sp.
XX
XX WO9749800-A1.
XX
PD 31-DEC-1997.
XX
PF 25-JUN-1997; 97WO-US010965.
XX
PR 25-JUN-1996; 96US-00672345.
XX
PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX Landry DW;
XX
DR WPI; 1998-077166/07.
XX
PT New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required in far
PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX
PS Claim 16; Page 73-74; 147pp; English.
XX
CC AAW39801-05 represent the amino acid sequences of the variable domain of
CC the Kappa light chain of catalytic antibodies which are able to degrade
CC cocaine. A series of cocaine transition state analogues (TSAs) were
CC prepared and used to immunise mice for production of hybridomas.
CC Catalytic antibodies were identified by their capacity to release 3H-
CC benzoic acid from 3H-phenyl cocaine. The 2A10 antibody (AAW39809
CC represents the heavy chain) was identified using TSA1, which is an
CC immunogenic conjugate of a phosphate monoester transition state analogue.
CC Antibody 2A10 has a per minute Kcat of 0.011. The antibodies reduce the
CC concentration of cocaine in a subject, and are used particularly for the
CC treatment of an overdose. They are also used for treating addiction (by
CC reducing the in vivo concentration that can be achieved)
XX
SQ Sequence 113 AA;

Query Match      100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82
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RESULT 15
ADI22125
ID ADI22125 standard; protein; 113 AA.
XX
AC ADI22125;
XX
DT 22-APR-2004 (first entry)
XX
DE Anti-platelet autoantibody related light chain amino acid L49 SEQ:88.
XX
KW anti-platelet autoantibody; autoantibody; blood clotting inhibition;
KW thrombus; platelet adhesion inhibition;
KW thrombotic thrombocytopenic purpura; platelet aggregation inhibition;
KW idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;
KW thrombolytic; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO2004005890-A2.
XX
PD 15-JAN-2004.
XX
PF 03-JUL-2003; 2003WO-US021304.
XX
PR 03-JUL-2002; 2002US-0394352P.
PR 18-SEP-2002; 2002US-0411694P.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
XX Siegel DL;
XX
DR WPI; 2004-142998/14.
XX
XX N-PSDB; ADI22072.
XX
PS Claim 12; SEQ ID NO 88; 232pp; English.
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The present invention describes a method (M1) for identifying an anti-platelet autoantibody (I) in a mammal. The autoantibody is detected by producing an antibody phage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that specifically binds with a platelet component, where the screening comprises panning the phage on intact platelets using competitive cell-surface panning. Also described: (1) an autoantibody identified by (M1); (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3) inhibiting (M2) blood clotting in a mammal having a thrombus or at risk of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a mammal having a thrombus or at risk of thrombus formation; (5) inhibiting (M4) binding of an anti-platelet autoantibody with a platelet component; (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6) thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7) platelet aggregation; (9) inhibiting (M8) platelet activation; (10) inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an anti-platelet autoantibody, or its biologically active fragment with a platelet; (12) identifying (M11) a peptide that inhibits binding of an anti-platelet autoantibody with a platelet; (13) a peptide identified by the method of (12); (14) a peptide that specifically binds with an anti-platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood clotting, inhibiting platelet aggregation, inhibiting platelet function or inhibiting platelet activation comprising an amount of an anti-platelet autoantibody, or its biologically active fragment that specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or its fragment comprises an antigen binding region derived from an H44L4 anti-platelet autoantibody, the kit further comprising a peptide inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator and an instructions for use. (I) has haemostatic, anticoagulant and thrombolytic activities. The autoantibodies (I) are useful for diagnosing and for developing therapeutics for diseases mediated by autoantibody binding with platelet antigens. (M6) and (M12) are useful for treating thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic purpura, respectively. (M2) and (M3) are useful for inhibiting blood

CC clotting. The present sequence is used in the exemplification of the
CC present invention.

XX
SQ Sequence 113 AA;

Query Match 100.0%; Score 33; DB 8; Length 113;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
| | | | |
Db 76 FTLEISR 82

Search completed: November 4, 2004, 00:47:41
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:48:50 ; Search time 72.3333 Seconds
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Title: US-09-712-819D-12
Perfect score: 33
Sequence: 1 FTLEISR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Published Applications AA:*

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- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	33	100.0	32	16	US-10-327-598-401
2	33	100.0	32	16	US-10-327-598-403
3	33	100.0	100	9	US-09-840-459-32
4	33	100.0	100	16	US-10-766-773-32
5	33	100.0	100	16	US-10-766-610-32
6	33	100.0	100	16	US-10-733-563-32
7	33	100.0	111	17	US-10-466-242-48
8	33	100.0	112	9	US-09-840-459-55
9	33	100.0	112	16	US-10-766-773-55
10	33	100.0	112	16	US-10-766-610-55
11	33	100.0	112	16	US-10-733-563-55
12	33	100.0	113	10	US-09-940-727B-5
13	33	100.0	113	10	US-09-940-727B-6

14	33	100.0	113	10	US-09-940-727B-7	Sequence 7, Appli
15	33	100.0	113	10	US-09-940-727B-8	Sequence 8, Appli
16	33	100.0	113	10	US-09-940-727B-100	Sequence 100, App
17	33	100.0	113	10	US-09-940-727B-104	Sequence 104, App
18	33	100.0	113	10	US-09-940-727B-108	Sequence 108, App
19	33	100.0	113	10	US-09-940-727B-112	Sequence 112, App
20	33	100.0	178	16	US-10-398-037-8	Sequence 8, Appli
21	33	100.0	280	10	US-09-940-727B-119	Sequence 119, App
22	33	100.0	348	14	US-10-335-394-12	Sequence 12, Appl
23	33	100.0	361	14	US-10-335-394-14	Sequence 14, Appl
24	30	90.9	329	14	US-10-369-493-13704	Sequence 13704, A
25	30	90.9	330	15	US-10-282-122A-67597	Sequence 67597, A
26	30	90.9	330	15	US-10-282-122A-69391	Sequence 69391, A
27	30	90.9	335	15	US-10-282-122A-55724	Sequence 55724, A
28	30	90.9	375	14	US-10-369-493-4199	Sequence 4199, Ap
29	29	87.9	32	10	US-09-563-222-80	Sequence 80, Appl
30	29	87.9	32	10	US-09-563-222-120	Sequence 120, App
31	29	87.9	32	10	US-09-947-839-71	Sequence 71, Appl
32	29	87.9	32	14	US-10-168-809-5	Sequence 5, Appli
33	29	87.9	32	16	US-10-663-244-49	Sequence 49, Appl
34	29	87.9	32	16	US-10-663-244-135	Sequence 135, App
35	29	87.9	32	16	US-10-327-598-385	Sequence 385, App
36	29	87.9	32	16	US-10-327-598-389	Sequence 389, App
37	29	87.9	32	17	US-10-783-950-80	Sequence 80, Appl
38	29	87.9	32	17	US-10-783-950-114	Sequence 114, Appl
39	29	87.9	93	9	US-09-905-243-61	Sequence 61, Appl
40	29	87.9	99	14	US-10-041-860-281	Sequence 281, App
41	29	87.9	99	14	US-10-041-860-323	Sequence 323, App
42	29	87.9	99	14	US-10-041-860-365	Sequence 365, App
43	29	87.9	99	14	US-10-308-817-176	Sequence 176, App
44	29	87.9	99	15	US-10-453-698-176	Sequence 176, App
45	29	87.9	100	9	US-09-822-698A-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-10-327-598-401
; Sequence 401, Application US/10327598
; Publication No. US20040181039A1
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; TITLE OF INVENTION: for Making and Using Them
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 401
; LENGTH: 32
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-401

Query Match 100.0%; Score 33; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 15 FTLEISR 21

RESULT 2

US-10-327-598-403
; Sequence 403, Application US/10327598

; Publication No. US20040181039A1									
; GENERAL INFORMATION:									
; APPLICANT: Krah, Eugene									
; APPLICANT: Guo, Honliang									
; APPLICANT: Aiyappa, Ashok									
; APPLICANT: Lawton, Robert									
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and									
; TITLE OF INVENTION: for Making and Using Them									
; FILE REFERENCE: 01-799-A									
; CURRENT APPLICATION NUMBER: US/10/327,598									
; CURRENT FILING DATE: 2002-12-20									
; PRIOR APPLICATION NUMBER: US 60/344,874									
; PRIOR FILING DATE: 2001-12-21									
; NUMBER OF SEQ ID NOS: 1139									
; SOFTWARE: PatentIn version 3.0									
; SEQ ID NO 403									
; LENGTH: 32									
; TYPE: PRT									
; ORGANISM: canis familiaris;									
US-10-327-598-403									
Query Match									
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Best Local Similarity 100.0%; Pred. No. 5.6;									
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; Sequence 32, Application US/09840459									
; Patent No. US20020150576A1									
; GENERAL INFORMATION:									
; APPLICANT: LaRosa, Gregory J.									
; APPLICANT: Horvath, Christopher									
; APPLICANT: Newman, Walter									
; APPLICANT: Jones, S. Tarran									
; APPLICANT: O'Brien, Siobhan H.									
; APPLICANT: O'Keefe, Theresa									
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND									
; TITLE OF INVENTION: METHODS OF USE THEREFOR									
; FILE REFERENCE: 1855.1052-012									
; CURRENT APPLICATION NUMBER: US/09/840,459									
; CURRENT FILING DATE: 2001-02-02									
; PRIOR APPLICATION NUMBER: PCT/US01/03537									
; PRIOR FILING DATE: 2001-02-02									
; PRIOR FILING DATE: 2000-02-03									
; PRIOR APPLICATION NUMBER: 09/497,625									
; PRIOR FILING DATE: 1999-07-22									
; PRIOR APPLICATION NUMBER: 09/359,193									
; PRIOR FILING DATE: 1999-07-22									
; PRIOR APPLICATION NUMBER: 09/121,781									
; PRIOR FILING DATE: 1998-07-23									
; NUMBER OF SEQ ID NOS: 107									
; SOFTWARE: FastSEQ for Windows Version 3.0									
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Db 76 FTLEISR 82									
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; Publication No. US20040126851A1									
; GENERAL INFORMATION:									
; APPLICANT: LaRosa, Gregory J.									
; APPLICANT: Horvath, Christopher									
; APPLICANT: Newman, Walter									
; APPLICANT: Jones, S. Tarran									
; APPLICANT: O'Brien, Siobhan H.									
; APPLICANT: O'Keefe, Theresa									
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; TITLE OF INVENTION: METHODS OF USE THEREFOR									
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; PRIOR FILING DATE: 1998-07-23									
; NUMBER OF SEQ ID NOS: 106									
; SOFTWARE: FastSEQ for Windows Version 3.0									
; SEQ ID NO 32									
; LENGTH: 100									
; TYPE: PRT									
; ORGANISM: Mus musculus									
US-10-766-773-32									
Query Match									
Best Local Similarity 100.0%; Score 33; DB 16; Length 100;									
Best Local Similarity 100.0%; Pred. No. 18;									
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY 1 FTLEISR 7									
Db 76 FTLEISR 82									
RESULT 5									
US-10-766-610-32									
; Sequence 32, Application US/10766610									
; Publication No. US20040132980A1									
; GENERAL INFORMATION:									
; APPLICANT: LaRosa, Gregory J.									
; APPLICANT: Horvath, Christopher									
; APPLICANT: Newman, Walter									
; APPLICANT: Jones, S. Tarran									
; APPLICANT: O'Brien, Siobhan H.									
; APPLICANT: O'Keefe, Theresa									
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND									
; TITLE OF INVENTION: METHODS OF USE THEREFOR									
; FILE REFERENCE: 1855.1052-029									
; CURRENT APPLICATION NUMBER: US/10/766,610									
; CURRENT FILING DATE: 2004-01-27									
; PRIOR APPLICATION NUMBER: 09/840,459									
; PRIOR FILING DATE: 2001-04-23									
; PRIOR APPLICATION NUMBER: PCT/US01/03537									
; PRIOR FILING DATE: 2001-02-02									
; PRIOR FILING DATE: 2000-02-03									
; PRIOR APPLICATION NUMBER: 09/497,625									
; PRIOR FILING DATE: 1999-07-22									
; PRIOR APPLICATION NUMBER: 09/359,193									
; PRIOR FILING DATE: 1999-07-22									
; PRIOR APPLICATION NUMBER: 09/121,781									
; PRIOR FILING DATE: 1998-07-23									
; NUMBER OF SEQ ID NOS: 107									
; SOFTWARE: FastSEQ for Windows Version 3.0									
; SEQ ID NO 32									
; LENGTH: 100									
; TYPE: PRT									
; ORGANISM: Mus musculus									
US-10-766-610-32									
Query Match									
Best Local Similarity 100.0%; Score 33; DB 16; Length 100;									
Best Local Similarity 100.0%; Pred. No. 18;									
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY 1 FTLEISR 7									
Db 76 FTLEISR 82									
RESULT 6									
US-10-766-610-32									
; Sequence 32, Application US/10766610									
; Publication No. US20040132980A1									
; GENERAL INFORMATION:									
; APPLICANT: LaRosa, Gregory J.									
; APPLICANT: Horvath, Christopher									
; APPLICANT: Newman, Walter									
; APPLICANT: Jones, S. Tarran									
; APPLICANT: O'Brien, Siobhan H.									
; APPLICANT: O'Keefe, Theresa									
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND									
; TITLE OF INVENTION: METHODS OF USE THEREFOR									
; FILE REFERENCE: 1855.1052-029									
; CURRENT APPLICATION NUMBER: US/10/766,610									
; CURRENT FILING DATE: 2004-01-27									
; PRIOR APPLICATION NUMBER: 09/840,459									
; PRIOR FILING DATE: 2001-04-23									
; PRIOR APPLICATION NUMBER: PCT/US01/03537									
; PRIOR FILING DATE: 2001-02-02									
; PRIOR FILING DATE: 2000-02-03									
; PRIOR APPLICATION NUMBER: 09/497,625									
; PRIOR FILING DATE: 1999-07-22									
; PRIOR APPLICATION NUMBER: 09/359,193									
; PRIOR FILING DATE: 1999-07-22									
; PRIOR APPLICATION NUMBER: 09/121,781									
; PRIOR FILING DATE: 1998-07-23									
; NUMBER OF SEQ ID NOS: 107									
; SOFTWARE: FastSEQ for Windows Version 3.0									
; SEQ ID NO 32									
; LENGTH: 100									
; TYPE: PRT									
; ORGANISM: Mus musculus									
US-10-766-610-32									
Query Match									
Best Local Similarity 100.0%; Score 33; DB 16; Length 100;									
Best Local Similarity 100.0%; Pred. No. 18;									
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY 1 FTLEISR 7									
Db 76 FTLEISR 82									
RESULT 7									
US-10-766-610-32									
; Sequence 32, Application US/10766610									
; Publication No. US20040132980A1									
; GENERAL INFORMATION:									
; APPLICANT: LaRosa, Gregory J.									
; APPLICANT: Horvath, Christopher									
; APPLICANT: Newman, Walter									
; APPLICANT: Jones, S. Tarran									
; APPLICANT: O'Brien, Siobhan H.									
; APPLICANT: O'Keefe, Theresa									
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND									
; TITLE OF INVENTION: METHODS OF USE THEREFOR									
; FILE REFERENCE: 1855.1052-029									
; CURRENT APPLICATION NUMBER: US/10/766,610									
; CURRENT FILING DATE: 2004-01-27									
; PRIOR APPLICATION NUMBER: 09/840,459									
; PRIOR FILING DATE: 2001-04-23									
; PRIOR APPLICATION NUMBER: PCT/US01/03537									
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; PRIOR FILING DATE: 2000-02-03									
; PRIOR APPLICATION NUMBER: 09/497,625									
; PRIOR FILING DATE: 1999-07-22									
; PRIOR APPLICATION NUMBER: 09/359,193									
; PRIOR FILING DATE: 1999-07-22									
; PRIOR APPLICATION NUMBER: 09/121,781									
; PRIOR FILING DATE: 1998-07-23									
; NUMBER OF SEQ ID NOS: 107									
; SOFTWARE: FastSEQ for Windows Version 3.0									
; SEQ ID NO 32									
; LENGTH: 100									
; TYPE: PRT									
; ORGANISM: Mus musculus									
US-10-766-610-32									
Query Match									
Best Local Similarity 100.0%; Score 33; DB 16; Length 100;									
Best Local Similarity 100.0%; Pred. No. 18;									
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY 1 FTLEISR 7									
Db 76 FTLEISR 82									
RESULT 8									
US-10-766-610-32									
; Sequence 32, Application US/10766610									
; Publication No. US20040132980A1									
; GENERAL INFORMATION:									
; APPLICANT: LaRosa, Gregory J.									
; APPLICANT: Horvath, Christopher									
; APPLICANT: Newman, Walter									
; APPLICANT: Jones, S. Tarran									
; APPLICANT: O'Brien, Siobhan H.									
; APPLICANT: O'Keefe, Theresa									
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND									
; TITLE OF INVENTION: METHODS OF USE THEREFOR									
; FILE REFERENCE: 1855.1052-029									
; CURRENT APPLICATION NUMBER: US/10/766,610									
; CURRENT FILING DATE: 2004-01-27									
; PRIOR APPLICATION NUMBER: 09/840,459									
; PRIOR FILING DATE: 2001-04-23									
; PRIOR APPLICATION NUMBER: PCT/US01/03537									
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; PRIOR FILING DATE: 2000-02-03									
; PRIOR APPLICATION NUMBER: 09/497,625									
; PRIOR FILING DATE: 1999-07-22									
; PRIOR APPLICATION NUMBER: 09/359,193									
; PRIOR FILING DATE: 1999-07-22									
; PRIOR APPLICATION NUMBER: 09/121,781									
; PRIOR FILING DATE: 1998-07-23									
; NUMBER OF SEQ ID NOS: 107									
; SOFTWARE: FastSEQ for Windows Version 3.0									
; SEQ ID NO 32									
; LENGTH: 100									
; TYPE: PRT									
; ORGANISM: Mus musculus									
US-10-766-610-32									
Query Match									
Best Local Similarity 100.0%; Score 33; DB 16; Length 100;									
Best Local Similarity 100.0%; Pred. No. 18;									
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY 1 FTLEISR 7									
Db 76 FTLEISR 82									
RESULT 9									
US-10-766-610-32									
; Sequence 32, Application US/10766610									
; Publication No. US20040132980A1									
; GENERAL INFORMATION:									
; APPLICANT: LaRosa, Gregory J.									
; APPLICANT: Horvath, Christopher									
; APPLICANT: Newman, Walter									
; APPLICANT: Jones, S. Tarran									
; APPLICANT: O'Brien, Siobhan H.									
; APPLICANT: O'Keefe, Theresa									
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND									
; TITLE OF INVENTION: METHODS OF USE THEREFOR									
; FILE REFERENCE: 1855.1052-029									
; CURRENT APPLICATION NUMBER: US/10/766,610									
; CURRENT FILING DATE: 2004-01-27									
; PRIOR APPLICATION NUMBER: 09/840,459									
; PRIOR FILING DATE: 2001-04-23									
; PRIOR APPLICATION NUMBER: PCT/US01/03537									
; PRIOR FILING DATE: 2001-02-02									
; PRIOR FILING DATE: 2000-02-03									
; PRIOR APPLICATION NUMBER: 09/497,625									
; PRIOR FILING DATE: 1999-07-22									
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; PRIOR APPLICATION NUMBER: 09/121,781									
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; SOFTWARE: FastSEQ for Windows Version 3.0									
; SEQ ID NO 32									
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; TYPE: PRT									
; ORGANISM: Mus musculus									
US-10-766-610-32									
Query Match									
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Best Local Similarity 100.0%; Pred. No. 18;									
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY 1 FTLEISR 7									
Db 76 FTLEISR 82									
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US-10-766-610-32									
; Sequence 32, Application US/10766610									
; Publication No. US20040132980A1									
; GENERAL INFORMATION:									
; APPLICANT: LaRosa, Gregory J.									
; APPLICANT: Horvath, Christopher									
; APPLICANT: Newman, Walter									
; APPLICANT: Jones, S. Tarran									
; APPLICANT: O'Brien, Siobhan H.									
; APPLICANT: O'Keefe, Theresa									
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND									
; TITLE OF INVENTION: METHODS OF USE THEREFOR									
; FILE REFERENCE: 1855.1052-029									
; CURRENT APPLICATION NUMBER: US/10/766,610									
; CURRENT FILING DATE: 2004-01-27									
; PRIOR APPLICATION NUMBER: 09/840,459									
; PRIOR FILING DATE: 2001-04-23									
; PRIOR APPLICATION NUMBER: PCT/US01/03537									
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; PRIOR FILING DATE: 2000-02-03									
; PRIOR APPLICATION NUMBER: 09/497,625									
; PRIOR FILING DATE: 1999-07-22									
; PRIOR APPLICATION NUMBER: 09/359,193									
; PRIOR FILING DATE: 1999-07-22									
; PRIOR APPLICATION NUMBER: 09/121,781									
; PRIOR FILING DATE: 1998-07-23									
; NUMBER OF SEQ ID NOS: 107									
; SOFTWARE: FastSEQ for Windows Version 3.0									
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; TYPE: PRT									
; ORGANISM: Mus musculus									
US-10-766-610-32									
Query Match									
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Best Local Similarity 100.0%; Pred. No. 18;									
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY 1 FTLEISR 7									
Db 76 FTLEISR 82									
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US-10-766-610-32									
; Sequence 32, Application US/10766610									
; Publication No. US20040132980A1									
; GENERAL INFORMATION:									
; APPLICANT: LaRosa, Gregory J.									
; APPLICANT: Horvath, Christopher									
; APPLICANT: Newman, Walter									
; APPLICANT: Jones, S. Tarran									
; APPLICANT: O'Brien, Siobhan H.									
; APPLICANT: O'Keefe, Theresa									
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND									
; TITLE OF INVENTION: METHODS OF USE THEREFOR									
; FILE REFERENCE: 1855.1052-029									
; CURRENT APPLICATION NUMBER: US/10/766,610									
; CURRENT FILING DATE: 2004-01-27									
; PRIOR APPLICATION NUMBER: 09/840,459									
; PRIOR FILING DATE: 2001-04-23									
; PRIOR APPLICATION NUMBER: PCT/US01/03537									
; PRIOR FILING DATE: 2001-02-02									
; PRIOR FILING DATE: 2000-02-03									
; PRIOR APPLICATION NUMBER: 09/497,625									
; PRIOR FILING DATE: 1999-07-22									
; PRIOR APPLICATION NUMBER: 09/359,193									
; PRIOR FILING DATE: 1999-07-22									
; PRIOR APPLICATION NUMBER: 09/121,781									
; PRIOR FILING DATE: 1998-07-23									
; NUMBER OF SEQ ID NOS: 107									
; SOFTWARE: FastSEQ for Windows Version 3.0									
; SEQ ID NO 32									
; LENGTH: 100									
; TYPE: PRT									
; ORGANISM: Mus musculus									
US-10-766-610-32									
Query Match									
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Best Local Similarity 100.0%; Pred. No. 18;									
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY 1 FTLEISR 7									
Db 76 FTLEISR 82									
RESULT 12									
US-10-766-610-32									
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; Publication No. US20040132980A1									
; GENERAL INFORMATION:									
; APPLICANT: LaRosa, Gregory J.									
; APPLICANT: Horvath, Christopher									
; APPLICANT: Newman, Walter									
; APPLICANT: Jones, S. Tarran									
; APPLICANT: O'Brien, Siobhan H.									
; APPLICANT: O'Keefe, Theresa									
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND									
; TITLE OF INVENTION: METHODS OF USE THEREFOR									
; FILE REFERENCE: 1855.1052-029									
; CURRENT APPLICATION NUMBER: US/10/766,610									
; CURRENT FILING DATE: 2004-01-27									
; PRIOR APPLICATION NUMBER: 09/840,459									
; PRIOR FILING DATE: 2001-04-23									
; PRIOR APPLICATION NUMBER: PCT/US01/03537									
; PRIOR FILING DATE: 2001-02-02									
; PRIOR FILING DATE: 2000-02-03									
; PRIOR APPLICATION NUMBER: 09/497,625									
; PRIOR FILING DATE: 1999-07-22									
; PRIOR APPLICATION NUMBER: 09/359,193									
; PRIOR FILING DATE: 1999-07-22									
; PRIOR APPLICATION NUMBER: 09/121,781									
; PRIOR FILING DATE: 1998-07-23									
; NUMBER OF SEQ ID NOS: 107									
; SOFTWARE: FastSEQ for Windows Version 3.0									
; SEQ ID NO 32									
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; TYPE: PRT									
; ORGANISM: Mus musculus									
US-10-766-610-32									
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Best Local Similarity 100.0%; Pred. No. 18;									
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY 1 FTLEISR 7									
Db 76 FTLEISR 82									
RESULT 13									
US-10-766-610-32									
; Sequence 32, Application US/10766610									
; Publication No. US20040132980A1									
; GENERAL INFORMATION:									
; APPLICANT: LaRosa, Gregory J.									
; APPLICANT: Horvath, Christopher									
; APPLICANT: Newman, Walter									
; APPLICANT: Jones, S. Tarran									
; APPLICANT: O'Brien, Siobhan H.									
; APPLICANT: O'Keefe, Theresa									
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND									
; TITLE OF INVENTION: METHODS OF USE THEREFOR									
; FILE REFERENCE: 1855.1052-029									
; CURRENT APPLICATION NUMBER: US/10/766,610									
; CURRENT FILING DATE: 2004-01-27									
; PRIOR APPLICATION NUMBER: 09/840,459									
; PRIOR FILING DATE: 2001-04-23									
; PRIOR APPLICATION NUMBER: PCT/US01/03537									
; PRIOR FILING DATE: 2001-02-02									
; PRIOR FILING DATE: 2000-02-03									
; PRIOR APPLICATION NUMBER: 09/497,625									
; PRIOR FILING DATE: 1999-07-22									
; PRIOR APPLICATION NUMBER: 09/359,193									
; PRIOR FILING DATE: 1999-07-22									
; PRIOR APPLICATION NUMBER: 09/121,781									
; PRIOR FILING DATE: 1998-07-23									
; NUMBER OF SEQ ID NOS: 107									
; SOFTWARE: FastSEQ for Windows Version 3.0									
; SEQ ID NO 32									
; LENGTH: 100									
; TYPE: PRT									
; ORGANISM: Mus musculus									
US-10-766-610-32									
Query Match									
Best Local Similarity 100.0%; Score 33; DB 16; Length 100;									
Best Local Similarity 100.0%; Pred. No. 18;									
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY 1 FTLEISR 7									
Db 76 FTLEISR 82									
RESULT 14									
US-10-766-610-32									
; Sequence 32, Application US/10766610									
; Publication No. US20040132980A1									
; GENERAL INFORMATION:									
; APPLICANT: LaRosa, Gregory J.									
; APPLICANT: Horvath, Christopher									
; APPLICANT: Newman, Walter									
; APPLICANT: Jones									

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
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Db 76 FTLEISR 82

RESULT 6
US-10-733-563-32
; Sequence 32, Application US/10733563
; Publication No. US20040151721A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Ponath, Paul
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-733-563-32

Query Match 100.0%; Score 33; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
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Db 76 FTLEISR 82

RESULT 7
US-10-466-242-48
; Sequence 48, Application US/10466242
; Publication No. US2004020887A1
; GENERAL INFORMATION:
; APPLICANT: Drakenberg, Katarina
; APPLICANT: Persson, Mats
; TITLE OF INVENTION: Materials and methods for treatment of hepatitis C
; FILE REFERENCE: 0380-P03248US00
; CURRENT APPLICATION NUMBER: US/10/466,242
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/SE02/00044
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(111)
; OTHER INFORMATION: Clone 2b:5 VK
US-10-466-242-48

Query Match 100.0%; Score 33; DB 17; Length 111;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
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Db 75 FTLEISR 81

RESULT 8
US-09-840-459-55
; Sequence 55, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-459-55

Query Match 100.0%; Score 33; DB 9; Length 112;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
|||||

Db 76 FTLEISR 82

RESULT 9
US-10-766-773-55
; Sequence 55, Application US/10766773
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-766-773-55

Query Match 100.0%; Score 33; DB 16; Length 112;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 10
US-10-766-610-55
; Sequence 55, Application US/10766610
; Publication No. US20040132980A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-029
; CURRENT APPLICATION NUMBER: US/10/766,610
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/840,459
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-766-610-55

Query Match 100.0%; Score 33; DB 16; Length 112;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 11
US-10-733-563-55
; Sequence 55, Application US/10733563
; Publication No. US20040151721A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Ponath, Paul
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 55
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-563-55

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Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 12
US-09-940-727B-5
; Sequence 5, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-5

Query Match 100.0%; Score 33; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 13
US-09-940-727B-6
; Sequence 6, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
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; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-6

Query Match 100.0%; Score 33; DB 10; Length 113;

Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Job time : 73.3333 secs

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 14
US-09-940-727B-7
; Sequence 7, Application US/09940727B
; Publication No. US20030077793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-7

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Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 15
US-09-940-727B-8
; Sequence 8, Application US/09940727B
; Publication No. US20030077793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-8

Query Match 100.0%; Score 33; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:44:39 ; Search time 286.667 Seconds
(without alignments)
27.056 Million cell updates/sec

Title: US-09-712-819D-12
Perfect score: 33
Sequence: 1 FTLEISR 7

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Searched: 6730630 seqs, 1107998698 residues

Total number of hits satisfying chosen parameters: 6730630

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA Main:*

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- 27: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

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1	33	100.0	7	21	US-09-712-819-12	Sequence 12, Appl
2	33	100.0	7	21	US-09-712-819D-12	Sequence 12, Appl
3	33	100.0	32	1	PCT-US04-20295-104	Sequence 104, App
4	33	100.0	32	1	PCT-US04-20564-104	Sequence 104, App
5	33	100.0	32	29	US-10-327-598-401	Sequence 401, App
6	33	100.0	32	29	US-10-327-598-403	Sequence 403, App
7	33	100.0	32	34	US-10-877-773-104	Sequence 104, App
8	33	100.0	32	34	US-10-877-774-104	Sequence 104, App
9	33	100.0	74	22	US-09-791-537-56094	Sequence 104, App
10	33	100.0	75	22	US-09-791-537-133183	Sequence 56094, A
11	33	100.0	100	1	PCT-US01-03537-32	Sequence 133183,
12	33	100.0	100	1	PCT-US03-39599A-32	Sequence 32, Appl
13	33	100.0	100	33	US-10-733-563-32	Sequence 32, Appl
14	33	100.0	100	33	US-10-766-610-32	Sequence 32, Appl
15	33	100.0	100	33	US-10-766-773-32	Sequence 32, Appl
16	33	100.0	104	23	US-09-834-366-18009	Sequence 18009, A
17	33	100.0	104	36	US-60-197-873-18009	Sequence 18009, A
18	33	100.0	111	30	US-10-466-242-48	Sequence 48, Appl
19	33	100.0	112	1	PCT-US01-03537-55	Sequence 55, Appl
20	33	100.0	112	1	PCT-US03-39599A-55	Sequence 55, Appl
21	33	100.0	112	1	PCT-US04-20295-19	Sequence 19, Appl
22	33	100.0	112	1	PCT-US04-20564-19	Sequence 19, Appl
23	33	100.0	112	33	US-10-733-563-55	Sequence 55, Appl
24	33	100.0	112	33	US-10-766-610-55	Sequence 55, Appl
25	33	100.0	112	33	US-10-766-773-55	Sequence 55, Appl
26	33	100.0	112	34	US-10-877-773-19	Sequence 19, Appl
27	33	100.0	112	34	US-10-877-774-19	Sequence 19, Appl
28	33	100.0	113	1	PCT-US03-21304-88	Sequence 88, Appl
29	33	100.0	113	1	PCT-US04-17118-14	Sequence 14, Appl
30	33	100.0	113	10	US-08-672-345A-5	Sequence 5, Appl
31	33	100.0	113	10	US-08-672-345A-6	Sequence 6, Appl
32	33	100.0	113	10	US-08-672-345A-7	Sequence 7, Appl
33	33	100.0	113	10	US-08-672-345A-8	Sequence 8, Appl
34	33	100.0	113	24	US-09-940-727B-5	Sequence 5, Appl
35	33	100.0	113	24	US-09-940-727B-6	Sequence 6, Appl
36	33	100.0	113	24	US-09-940-727B-7	Sequence 7, Appl
37	33	100.0	113	24	US-09-940-727B-8	Sequence 8, Appl
38	33	100.0	113	24	US-09-940-727B-100	Sequence 100, App
39	33	100.0	113	24	US-09-940-727B-104	Sequence 104, App
40	33	100.0	113	24	US-09-940-727B-108	Sequence 108, App
41	33	100.0	113	24	US-09-940-727B-112	Sequence 112, App
42	33	100.0	119	26	US-10-049-868-3	Sequence 3, Appl
43	33	100.0	119	26	US-10-049-868A-3	Sequence 3, Appl
44	33	100.0	121	3	US-07-868-983-6	Sequence 6, Appl
45	33	100.0	122	1	PCT-US99-24443-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-712-819-12
; Sequence 12, Application US/09712819
; GENERAL INFORMATION:
; APPLICANT: Stevens, Fred J.
; Argon, Yair
; Davis, David P.
; Raffan, Rosemarie
; TITLE OF INVENTION: Fibril-Blocking Peptide, A Method for Preventing
; Fibril Formation
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESS: CHERSKOV & FLAYNIK
; STREET: 20 N. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606
; COMPUTER READABLE FORM: CD-R, 700 MB storage

COMPUTER: PC
OPERATING SYSTEM: Microsoft Windows XP
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/712,819
FILING DATE: 13-Nov-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 60/165,424
FILING DATE: 1999-NOV-14
ATTORNEY/AGENT INFORMATION:
NAME: Cherskov, Michael J.
REGISTRATION NUMBER: 33,664
REFERENCE/DOCKET NUMBER: 0003/00537
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 621-1330
TELEFAX: (312) 621-0088
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-712-819-12

Query Match 100.0%; Score 33; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 1 FTLEISR 7

RESULT 2
US-09-712-819D-12
Sequence 12, Application US/09712819D
GENERAL INFORMATION:
APPLICANT: Stevens, Fred J.
Davis, Yair
Raffen, Rosemarie
TITLE OF INVENTION: Fibril-Blocking Peptide, A Method for Preventing
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHERSKOV & FLAYNIK
STREET: 20 N. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R, 700 MB storage
COMPUTER: PC
OPERATING SYSTEM: Microsoft Windows XP
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/712,819D
FILING DATE: 13-Nov-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 60/165,424
FILING DATE: 1999-NOV-14
ATTORNEY/AGENT INFORMATION:
NAME: Cherskov, Michael J.
REGISTRATION NUMBER: 33,664
REFERENCE/DOCKET NUMBER: 0003/00537
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 621-1330
TELEFAX: (312) 621-0088
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids

TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-712-819D-12

Query Match 100.0%; Score 33; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 1 FTLEISR 7

RESULT 3
PCT-US04-20295-104
Sequence 104, Application PC/TUS0420295
GENERAL INFORMATION:
APPLICANT: AGENIX, INC.
APPLICANT: Weber, Richard
APPLICANT: Feng, Xiao
APPLICANT: Foord, Orit
APPLICANT: Green, Larry
APPLICANT: Gudas, Jean
APPLICANT: Keyt, Bruce
APPLICANT: Liu, Ying
APPLICANT: Rathanaswami, Palani
APPLICANT: Raya, Robert
APPLICANT: Yang, Xiao Dong
APPLICANT: Corvalan, Jose
APPLICANT: Foltz, Ian
APPLICANT: Jia, Xiao-Chi
APPLICANT: Kang, Jaspal
APPLICANT: King, Chadwick T.
APPLICANT: Klakamp, Scott L.
APPLICANT: Su, Qiaojuan Jane
TITLE OF INVENTION: ANTIBODIES DIRECTED TO THE DELETION
TITLE OF INVENTION: MUTANTS OF EPIDERMAL GROWTH FACTOR RECEPTOR AND USES THEREOF
FILE REFERENCE: AGENIX.087VPC
CURRENT APPLICATION NUMBER: PCT/US04/20295
CURRENT FILING DATE: 2004-07-02
PRIOR APPLICATION NUMBER: US 60/483,145
PRIOR FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: US 60/525,570
PRIOR FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US 60/562,453
PRIOR FILING DATE: 2004-04-15
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 104
LENGTH: 32
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide sequence
PCT-US04-20295-104

Query Match 100.0%; Score 33; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 15 FTLEISR 21

RESULT 4
PCT-US04-20564-104
Sequence 104, Application PC/TUS0420564
GENERAL INFORMATION:
APPLICANT: AGENIX, INC.
APPLICANT: Weber, Richard

```
; APPLICANT: Feng, Xiao
; APPLICANT: Foord, Orit
; APPLICANT: Green, Larry
; APPLICANT: Gudas, Jean
; APPLICANT: Keyt, Bruce
; APPLICANT: Liu, Ying
; APPLICANT: Rathanaswami, Palani
; APPLICANT: Raya, Robert
; APPLICANT: Yang, Xiao Dong
; APPLICANT: Corvalan, Jose
; APPLICANT: Foltz, Ian
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Kang, Jaspal
; APPLICANT: King, Chadwick T.
; APPLICANT: Klakamp, Scott L.
; APPLICANT: Su, Qiaojuan Jane
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO THE DELETION
; TITLE OF INVENTION: MUTANTS OF EPIDERMAL GROWTH FACTOR RECEPTOR AND USES THEREOF
; FILE REFERENCE: ABGENIX.087VPC2
; CURRENT APPLICATION NUMBER: PCT/US04/20564
; CURRENT FILING DATE: 2004-07-06
; PRIOR APPLICATION NUMBER: US 60/483,145
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 60/525,570
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/562,453
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide sequence
PCT-US04-20564-104
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Query Match 100.0%; Score 33; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 FTLEISR 7
Db 15 FTLEISR 21
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RESULT 5
US-10-327-598-401
; Sequence 401, Application US/10327598
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; TITLE OF INVENTION: for Making and Using Them
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 401
; LENGTH: 32
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-401
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Best Local Similarity 100.0%; Pred. No. 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 FTLEISR 7
Db 15 FTLEISR 21

RESULT 6
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; Sequence 403, Application US/10327598
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, an
; TITLE OF INVENTION: for Making and Using Them
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 403
; LENGTH: 32
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-403
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 FTLEISR 7
Db 15 FTLEISR 21
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RESULT 7
US-10-877-773-104
; Sequence 104, Application US/10877773
; GENERAL INFORMATION:
; APPLICANT: Weber, Richard
; APPLICANT: Feng, Xiao
; APPLICANT: Foord, Orit
; APPLICANT: Green, Larry
; APPLICANT: Gudas, Jean
; APPLICANT: Keyt, Bruce
; APPLICANT: Liu, Ying
; APPLICANT: Rathanaswami, Palani
; APPLICANT: Raya, Robert
; APPLICANT: Yang, Xiao Dong
; APPLICANT: Corvalan, Jose
; APPLICANT: Foltz, Ian
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Kang, Jaspal
; APPLICANT: King, Chadwick T.
; APPLICANT: Klakamp, Scott L.
; APPLICANT: Su, Qiaojuan Jane
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO THE DELETION
; TITLE OF INVENTION: MUTANTS OF EPIDERMAL GROWTH FACTOR RECEPTOR AND USES THEREOF
; FILE REFERENCE: ABGENIX.087A
; CURRENT APPLICATION NUMBER: US/10/877,773
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: 60/483,145
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/525,570
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/562,453
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 32
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide sequence
US-10-877-773-104

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Query Match      100.0%; Score 33; DB 34; Length 32;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1 FTLEISR 7
      |||||
Db      15 FTLEISR 21

```

```

RESULT 8
US-10-877-774-104
; Sequence 104, Application US/10877774
; GENERAL INFORMATION:
; APPLICANT: Weber, Richard
; APPLICANT: Feng, Xiao
; APPLICANT: Foord, Orit
; APPLICANT: Green, Larry
; APPLICANT: Gudas, Jean
; APPLICANT: Keyt, Bruce
; APPLICANT: Liu, Ying
; APPLICANT: Rathanaswami, Palani
; APPLICANT: Raya, Robert
; APPLICANT: Yang, Xiao Dong
; APPLICANT: Corvalan, Jose
; APPLICANT: Foltz, Ian
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Kang, Jaspal
; APPLICANT: King, Chadwick T.
; APPLICANT: Klakamp, Scott L.
; APPLICANT: Su, Qiaojuan Jane

```

```

; TITLE OF INVENTION: ANTIBODIES DIRECTED TO THE DELETION
; FILE REFERENCE: ABGENIX.087A2
; CURRENT APPLICATION NUMBER: US/10/877,774
; CURRENT FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: 60/483,145
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/525,570
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/562,453
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide sequence
US-10-877-774-104

```

```

Query Match      100.0%; Score 33; DB 34; Length 32;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 FTLEISR 7
      |||||
Db      15 FTLEISR 21

```

```

RESULT 9
US-09-791-537-56094
; Sequence 56094, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph

```

```

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 56094
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-56094

```

```

Query Match      100.0%; Score 33; DB 22; Length 74;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 FTLEISR 7
      |||||
Db      45 FTLEISR 51

```

```

RESULT 10
US-09-791-537-133183
; Sequence 133183, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph

```

```

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 133183
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-133183

```

```

Query Match      100.0%; Score 33; DB 22; Length 75;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 FTLEISR 7
      |||||
Db      51 FTLEISR 57

```

```

RESULT 11
PCT-US01-03537-32
; Sequence 32, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23

```


; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-32

Query Match 100.0%; Score 33; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
|||||
Db 76 FTLEISR 82

RESULT 12

PCT-US03-39599A-32
; Sequence 32, Application PC/TUS0339599A
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 10448-213W01
; CURRENT APPLICATION NUMBER: PCT/US03/39599A
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US03-39599A-32

Query Match 100.0%; Score 33; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
|||||
Db 76 FTLEISR 82

RESULT 13

US-10-733-563-32
; Sequence 32, Application US/10733563
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Ponath, Paul
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-733-563-32

Query Match 100.0%; Score 33; DB 33; Length 100;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
|||||
Db 76 FTLEISR 82

RESULT 14

US-10-766-610-32
; Sequence 32, Application US/10766610
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-029
; CURRENT APPLICATION NUMBER: US/10/766,610
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/840,459
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-766-610-32

Query Match 100.0%; Score 33; DB 33; Length 100;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
|||||
Db 76 FTLEISR 82

RESULT 15

US-10-766-773-32
; Sequence 32, Application US/10766773
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT

; ORGANISM: Mus musculus
US-10-766-773-32

Query Match 100.0%; Score 33; DB 33; Length 100;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLEISR 7
| | | | |
Db 76 FTLEISR 82

Search completed: November 4, 2004, 01:09:18
Job time : 287.667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 07:01:08 ; Search time 38 Seconds
(without alignments)
17.724 Million cell updates/sec

Title: US-09-712-819D-6
Perfect score: 33
Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	15	45.5	7	2 S19630	ribosomal protein
2	13	39.4	7	2 A28709	phosphonoacetaldeh
3	12	36.4	5	2 T14910	hypothetical prote
4	11	33.3	5	2 PT0644	T-cell receptor be
5	10	30.3	7	2 PS0254	18K protein 5507 -
6	9	27.3	3	3 T13892	cytochrome-c oxida
7	9	27.3	4	2 T46627	hypothetical prote
8	9	27.3	4	2 I40804	endoglucanase F -
9	9	27.3	5	2 A44955	alkanal monooxygen
10	9	27.3	5	2 S11127	phosphoprotein, bo
11	9	27.3	5	2 PT0525	T-cell receptor be
12	9	27.3	5	2 PT0577	T-cell receptor be
13	9	27.3	5	2 PT0700	T-cell receptor be
14	9	27.3	5	2 S69237	surface protein te
15	9	27.3	5	2 A60521	glycogen phosphory
16	9	27.3	5	2 E42364	flagellar protein
17	9	27.3	5	2 PT0565	T-cell receptor be
18	9	27.3	6	2 A60986	N-formyl oligopept
19	9	27.3	6	2 A43766	28K ubiquitin-immu
20	9	27.3	6	2 I37263	Y protein - human
21	9	27.3	6	2 B26206	alpha-1,4-glucan-p
22	9	27.3	6	2 I65546	MHC H2-L antigen -
23	9	27.3	6	2 PT0518	T-cell receptor be
24	9	27.3	6	2 PT0662	T-cell receptor be
25	9	27.3	6	2 I49424	cytotoxic T-lympho
26	9	27.3	7	2 JN0859	peptidyl-dipeptida
27	9	27.3	7	2 B39127	phosphotransferase
28	9	27.3	7	2 S25266	p1E protein - Esc
29	9	27.3	7	2 PN0150	omega-gliadine 1'

30	9	27.3	7	2 S78024	ribosomal protein
31	9	27.3	7	2 E48394	glycoprotein compo
32	9	27.3	7	2 I48086	DNA topoisomerase
33	9	27.3	7	2 PT0671	T-cell receptor be
34	9	27.3	7	2 S66442	glutathione S-stran
35	9	27.3	7	2 B48394	major fat-globule
36	9	27.3	7	2 PN0649	pullulanase (EC 3.
37	9	27.3	7	2 S09066	globulin IV alpha
38	9	27.3	7	2 A15398	choline oxidase (E
39	9	27.3	7	2 A25269	sex pheromone CAM3
40	9	27.3	7	2 A30812	sex pheromone CCF1
41	8	24.2	4	2 I40505	hypothetical prote
42	8	24.2	5	2 I39964	ribosomal protein
43	8	24.2	5	2 I39966	ribosomal protein
44	8	24.2	5	2 I39965	ribosomal protein
45	8	24.2	5	2 B22565	R-phycoerythrin al

ALIGNMENTS

RESULT 1

S19630
ribosomal protein L30 - Streptomyces griseus (fragment)
C;Species: Streptomyces griseus
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 06-Jun-1997
C;Accession: S19630
R;Ochi, K.
Int. J. Syst. Bacteriol. 42, 144-150, 1992
A;Title: Electrophoretic heterogeneity of ribosomal protein AT-L30 among actinomycete g
A;Reference number: S19630; MUID:92144363; PMID:1736962
A;Accession: S19630
A;Molecule type: protein
A;Residues: 1-7 <OCH>
A;Experimental source: strain IFO 13189
C;Superfamily: Escherichia coli ribosomal protein L30
C;Keywords: protein biosynthesis; ribosome

Query Match 45.5%; Score 15; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LKISR 7
Db 3 LKITQ 7

RESULT 2

A28709
phosphonoacetaldehyde hydrolase - Bacillus cereus (fragment)
C;Species: Bacillus cereus
C;Date: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 30-Sep-1993
C;Accession: A28709
R;Olsen, D.B.; Hepburn, T.W.; Moos, M.; Mariano, P.S.; Dunaway-Mariano, D.
Biochemistry 27, 2229-2234, 1988
A;Title: Investigation of the Bacillus cereus phosphonoacetaldehyde hydrolase. Evidence
idue.
A;Reference number: A28709; MUID:88241058; PMID:3132206
A;Accession: A28709
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <OLS>

Query Match 39.4%; Score 13; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LKI 5
Db 1 LKI 3

RESULT 3

T14910
hypothetical protein - parsley
C;Species: Petroselinum crispum (parsley)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T14910
R;Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.
Mol. Gen. Genet. 257, 595-605, 1998
A;Title: CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis of
A;Reference number: Z18261; MUID:98265918; PMID:9604882
A;Accession: T14910
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-5 <KIR>
A;Cross-references: EMBL:Y10810; NID:g3336904; PIDN:CAA71769.1; PID:g3336905
A;Experimental source: ssp. Hamburger Schnitt

Query Match 36.4%; Score 12; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISR 7
:|:
DB 2 VSR 4

RESULT 4
PT0644
T-cell receptor beta chain V-D-J region (111-1G) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: PT0644
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0644
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Cross-references: UNIPROT:Q9Z2T6
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 33.3%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2
||
DB 4 FT 5

RESULT 5
PS0254
18K protein 5507 - rice (strain Nihonbare) (fragment)
C;Species: Oryza sativa (rice)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Mar-1995
C;Accession: PS0254
R;Tsugita, A.
submitted to JIPID, April 1993
A;Reference number: PS0206
A;Accession: PS0254
A;Molecule type: protein
A;Residues: 1-7 <TSU>
A;Experimental source: leaf, chloroplast, strain Nihonbare
A;Note: molecular weight 18k, pI 4.4

Query Match 30.3%; Score 10; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 LKISR 7
|:|:

Db 1 LAIAK 5

RESULT 6
T13892
cytochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrion (fra
C;Species: mitochondrion Lampetra fluviatilis (river lamprey)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: T13892
R;Delarbre, C.; Barriol, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol. 14, 807-813, 1997
A;Title: The main features of the craniate mitochondrial DNA between the ND1 and the CO
A;Reference number: Z17775; MUID:97398704; PMID:9254918
A;Accession: T13892
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3
A;Cross-references: EMBL:Y09528; NID:g2340016; PIDN:CAA70721.1; PID:g4379123
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match 27.3%; Score 9; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
||
DB 2 TL 3

RESULT 7
T46627
hypothetical protein c4 - loblolly pine
C;Species: Pinus taeda (loblolly pine)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C;Accession: T46627
R;Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
submitted to the EMBL Data Library, July 1995
A;Description: Cloning of a chitinase homolog which lacks chitin binding sites and is
A;Reference number: Z23105
A;Accession: T46627
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-4 <CHA>
A;Cross-references: EMBL:U31309; NID:g974285; PID:g974292
A;Experimental source: strain s6PT2xs6PT3; 8 month seedlings

Query Match 27.3%; Score 9; DB 2; Length 4;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LKI 5
:|:
DB 1 MKL 3

RESULT 8
I40804
endoglucanase F - Clostridium thermocellum (fragment)
C;Species: Clostridium thermocellum
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40804
R;Mishra, S.; Beguin, P.; Aubert, J.
J. Bacteriol. 173, 80-85, 1991
A;Title: Transcription of clostridium thermocellum endoglucanase genes celf and celd.
A;Reference number: I40804; MUID:91100322; PMID:1987137
A;Accession: I40804
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-4 <RES>
A;Cross-references: UNIPROT:P26224; GB:M64363; NID:g144771

C;Genetics:

A;Gene: celf

A;Start codon: TTG

Query Match

27.3%; Score 9; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KI 5

||

3 KI 4

RESULT 9

A44955

alkanal monooxygenase (FMN-linked) (EC 1.14.14.3) alpha chain - Vibrio harveyi (fragment)

C;Species: Vibrio harveyi

C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-May-2000

C;Accession: A44955

R;Paquette, O.; Tu, S.C.

Photochem. Photobiol. 50, 817-825, 1989

A;Title: Chemical modification and characterization of the alpha cysteine 106 at the Vib

A;Reference number: A44955; MUID:90175700; PMID:2626493

A;Accession: A44955

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5 <PAQ>

C;Keywords: FMN; luminescence; monooxygenase; oxidoreductase

Query Match

27.3%; Score 9; DB 2; Length 5;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ISR 7

||

3 IXR 5

RESULT 10

S11127

phosphoprotein, bone - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Mar-2000

C;Accession: S11127; S11128

R;Mikuni-Takagaki, Y.; Glimcher, M.J.

Biochem. J. 268, 585-591, 1990

A;Title: Post-translational processing of chicken bone phosphoproteins. Identification o

A;Reference number: S11127; MUID:90303246; PMID:2363696

A;Accession: S11127

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5 <MIK1>

A;Accession: S11128

A;Status: preliminary

A;Molecule type: protein

A;Residues: 'X', 2-5 <MIK2>

C;Keywords: phosphoprotein

Query Match

27.3%; Score 9; DB 2; Length 5;

Best Local Similarity 33.3%; Pred. No. 2.8e+05;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISR 7

||

3 VSK 5

RESULT 11

PT0525

T-cell receptor beta chain V-D-J region (100-4J) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0525

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0525

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-5 <FEE>

A;Experimental source: adult thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match

27.3%; Score 9; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SR 7

||

2 SR 3

RESULT 12

PT0577

T-cell receptor beta chain V-D-J region (141-1BC) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0577; PT0574

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0577

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-5 <FEE>

A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-1BC

A;Accession: PT0574

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-5 <FE2>

A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-1Q

C;Keywords: T-cell receptor

Query Match

27.3%; Score 9; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SR 7

||

3 SR 4

RESULT 13

PT0700

T-cell receptor beta chain V-D-J region (161-2A) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0700

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0700

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-5 <FEE>

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match

27.3%; Score 9; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SR 7

Db ||
3 SR 4

RESULT 14
S69237
surface protein tetrabrachion heavy chain - Staphylothermus marinus (fragment)
C;Species: Staphylothermus marinus
C;Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 17-Mar-1999
C;Accession: S69237
R;Peters, J.; Nitsch, M.; Kuehlmoegen, B.; Golbik, R.; Lupas, A.; Kellermann, J.; Engelh
J. Mol. Biol. 245, 385-401, 1995
A;Title: Tetrabrachion: a filamentous archaeobacterial surface protein assembly of unusua
A;Reference number: S69237; MUID:95139068; PMID:7837271
A;Accession: S69237
A;Molecule type: protein
A;Residues: 1-5 <PET>
A;Experimental source: strain F1, DSM 3639
C;Keywords: cell wall; glycoprotein; heat-stable protein

Query Match 27.3%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
||
Db 2 TL 3

RESULT 15
A60521
glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
N;Alternate names: glycogen phosphorylase b
C;Species: Liza ramada
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Mar-2004
C;Accession: A60521
R;Bonamusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A;Title: Purification and characterization of glycogen phosphorylase B from skeletal mus
A;Reference number: A60521; MUID:90227907; PMID:2109669
C;Accession: A60521
A;Molecule type: protein
A;Residues: 1-5 <BON>
C;Keywords: glycosyltransferase; hexosyltransferase; phosphorylase b kinase
F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experim

Query Match 27.3%; Score 9; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KIS 6
: ||
Db 1 QIS 3

Search completed: November 4, 2004, 07:10:22
Job time : 39 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 4, 2004, 06:53:12 ; Search time 188 Seconds
(without alignments)
21.424 Million cell updates/sec

Title: US-09-712-819D-6
Perfect score: 33
Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 167

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	13	39.4	6	P82181	P82181 spinacia ol
2	13	39.4	6	P82182	P82182 spinacia ol
3	11	33.3	5	RE31_LITRU	P82072 litoria rub
4	11	33.3	5	RE32_LITRU	P82073 litoria rub
5	11	33.3	7	Q95945	Q95945 saccharomyc
6	11	33.3	7	P83530	P83530 lactobacill
7	10	30.3	6	P82541	P82541 spinacia ol
8	10	30.3	7	GFRP_MOUSE	P99025 mus musculu
9	9	27.3	4	Q08433	Q08433 rattus sp.
10	9	27.3	5	UF01_MOUSE	P38639 mus musculu
11	9	27.3	6	UN06_CLOPA	P81351 clostridium
12	9	27.3	7	CCF1_ENTFA	P20104 enterococcu
13	9	27.3	7	CHOX_ALCSP	P16101 alcaligenes
14	9	27.3	7	CIA_ENTFA	P11932 enterococcu
15	9	27.3	7	UC24_MAIZE	P80630 zea mays (m
16	9	27.3	7	Q15897	Q15897 homo sapien
17	9	27.3	7	Q93233	Q93233 lycopersico
18	9	27.3	7	O07354	O07354 synecococc
19	9	27.3	7	Q8GL00	Q8GL00 borrelia bu
20	9	27.3	7	Q8GL04	Q8GL04 borrelia bu
21	9	27.3	7	Q8GL12	Q8GL12 borrelia bu
22	9	27.3	7	O55184	O55184 rattus norv
23	9	27.3	7	Q63480	Q63480 rattus norv
24	9	27.3	7	Q8K3H6	Q8K3H6 rattus norv
25	9	27.3	7	Q8JE81	Q8JE81 human immun
26	8	24.2	5	AL14_CARMA	P81817 carcinus ma
27	8	24.2	5	PSK_DAUCA	P58261 daucus caro
28	8	24.2	7	ALL2_CARMA	P81805 carcinus ma
29	8	24.2	7	ALL3_CARMA	P81806 carcinus ma
30	8	24.2	7	ALL4_CARMA	P81807 carcinus ma
31	8	24.2	7	ALL5_CARMA	P81808 carcinus ma

32	8	24.2	7	1	ALL7_CVDPO	P82158 cydia pomon
33	8	24.2	7	1	CARP_MYTED	P10420 mytilus edu
34	8	24.2	7	1	FAR5_HIRME	P42564 hirudo medi
35	8	24.2	7	2	P70804	P70804 azotobacter
36	8	24.2	7	2	Q47029	Q47029 enterobacte
37	8	24.2	7	2	Q9YIQ9	Q9YIQ9 human adeno
38	8	24.2	7	2	Q9YI0	Q9YI0 human adeno
39	8	24.2	7	2	Q9YVE3	Q9YVE3 human adeno
40	7	21.2	3	1	LUXE_VIBFI	P24272 vibrio fisc
41	7	21.2	5	2	P83073	P83073 bacillus ce
42	7	21.2	6	1	LOK1_LOCOMI	P41491 locusta mig
43	7	21.2	6	1	VP19_HHV1K	P23210 human herpe
44	7	21.2	7	2	Q8NH7	Q8nhh7 homo sapien
45	7	21.2	7	2	Q8TAQ4	Q8taq4 homo sapien

ALIGNMENTS

RESULT 1

P82181
ID P82181 PRELIMINARY; PRT; 6 AA.
AC P82181;
DT 01-JUN-2000 (Tremblrel. 14, Created)
DT 01-JUN-2000 (Tremblrel. 14, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 beta (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. ALWARO; TISSUE=Leaf;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 kDa.
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0019843; F:rRNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro; IPR002363; Ribosomal_L10eub.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KW Chloroplast; Ribosomal protein; rRNA-binding.
FT NON TER 6
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 39.4%; Score 13; DB 2; Length 6;
Best Local Similarity 100.0%; Pred.No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ISR 7
Db 2 ISR 4

RESULT 2

P82182
ID P82182 PRELIMINARY; PRT; 6 AA.
AC P82182;
DT 01-JUN-2000 (Tremblrel. 14, Created)
DT 01-JUN-2000 (Tremblrel. 14, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 gamma (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. ALVARO; TISSUE=Leaf;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 kDa.
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR GO: GO:0009507; C:chloroplast; IEA.
DR GO: GO:0019843; F:rRNA binding; IEA.
DR GO: GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro: IPR002363; Ribosomal_L10eub.
DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
KW Chloroplast; Ribosomal protein; rRNA-binding.
FT NON TER 6
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 39.4%; Score 13; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISR 7
Db 2 ISR 4

RESULT 3
RE31 LITRU STANDARD; PRT; 5 AA.
AC P82072;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
'Litoria rubella'. The skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAB; RANGE=1-5; NOTE=Ref.1.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
FT MOD RES 5
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 33.3%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2
Db 4 FT 5

RESULT 4
RE32 LITRU STANDARD; PRT; 5 AA.
AC P82073;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rubellidin 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
Litoria electrica. Comparison with the skin peptides from Litoria
rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
KW Amphibian defense peptide; Direct protein sequencing.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 33.3%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2
Db 4 FT 5

RESULT 5
Q95945 PRELIMINARY; PRT; 7 AA.
AC Q95945;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inside intron 5 (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D273-10B;
RX MEDLINE=81069885; PubMed=6254986;
RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
RT "Assembly of the mitochondrial membrane system: Structure and
nucleotide sequence of the gene coding for subunit 1 of yeast
cytochrome oxidase.";
RL J. Biol. Chem. 255:11927-11941(1980).
DR EMBL; V00694; CAA24066.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;

Query Match 33.3%; Score 11; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KIS 6
Db 5 KLS 7


```
RESULT 6
P83530 PRELIMINARY; PRT; 7 AA.
ID P83530
AC P83530; (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Unknown protein from 2D-page (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 20451;
RX PubMed=12112860;
RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
RT "High pressure effects step-wise altered protein expression in
  Lactobacillus sanfranciscensis.";
RL Proteomics 2:765-774(2002).
CC -!- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
  protein is: 15 kDa.
CC NON_TER 1 1
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 790 MW; 6AAB02CAA731B2A0 CRC64;

Query Match 33.3%; Score 11; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLKI 5
DB 2 TLDV 5

RESULT 7
P82541 PRELIMINARY; PRT; 6 AA.
ID P82541
AC P82541;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chloroplast 30S ribosomal protein S19 beta (Fragment).
OS Spinacia oleracea (Spinach).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC STRAIN=cv. ALVARO; TISSUE=Leaf;
RX MEDLINE=20435797; PubMed=10874039;
RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
  the small subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 37:28455-28465(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
CC -!- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
CC -!- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA
  FORM IS THE MINOR BASIC FORM.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 kDa.
CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
DR GO:0009507; C:chloroplast; IEA.
DR GO:0019843; F:rRNA binding; IEA.
DR GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro: IPR002222; Ribosomal S19.
DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL.

KW Chloroplast; Ribosomal protein; rRNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;

Query Match 30.3%; Score 10; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLK 4
DB 3 SLK 5

RESULT 8
GFRP_MOUSE STANDARD; PRT; 7 AA.
ID GFRP_MOUSE
AC P99025;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).
GN Name=Gchfr; Synonyms=Gfrp;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,
  Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F., Cowthorne M.;
RL Submitted (AUG-1998) to Swiss-Prot.
CC -!- FUNCTION: Mediates tetrahydrobiopterin inhibition of GTP
  cyclohydrolase I. This inhibition is reversed by L-phenylalanine
  (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
DR SWISS-2DPAGE; P99025; MOUSE.
KW Direct protein sequencing.
FT INIT_MET 0 0
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 806 MW; 71B5B057273B4700 CRC64;

Query Match 30.3%; Score 10; DB 1; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LKIS 6
DB 3 LLIS 6

RESULT 9
Q08433 PRELIMINARY; PRT; 4 AA.
ID Q08433
AC Q08433;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Bilirubin UDP-glucuronosyltransferase (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gunn;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koiwai O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
  hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
DR EMBL; S38636; AAB19259.1; -.
DR GO:0016740; F:transferase activity; IEA.
```

KW Transferase. 4 4 473 MW; 633732C420000000 CRC64;
FT NON TER 4 4 473 MW; 633732C420000000 CRC64;
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 27.3%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LK 4
Db 3 LK 4

RESULT 10
UF01_MOUSE STANDARD; PRT; 5 AA.
ID UF01_MOUSE
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of fibroblasts (P19) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast; PubMed=7523108;
RX MEDLINE=9500907; Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins using
RT preparative two-dimensional gel electrophoresis."
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.6, its MW is: 19 kDa.
KW Direct protein sequencing.
FT NON TER 5
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ISR 7
Db 2 IGR 4

RESULT 11
UN06_CLOPA STANDARD; PRT; 6 AA.
ID UN06_CLOPA
AC P81351;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein CP 6 from 2D-PAGE (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5."
RL Electrophoresis 19:802-806(1998).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.0, its MW is: 75.9 kDa.
KW Direct protein sequencing.
FT NON TER 6
SQ SEQUENCE 6 AA; 657 MW; 605B1DC1A45A8000 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLKI 5
Db 3 TAEI 6

RESULT 12
CCF1_ENTFA STANDARD; PRT; 7 AA.
ID CCF1_ENTFA
AC P20104;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sex pheromone CCF10.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=89008313; PubMed=3139658;
RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
RA Adsit J.C., Dunny G.M., Suzuki A.;
RT "Structure of CCF10, a peptide sex pheromone which induces conjugative
RT transfer of the Streptococcus faecalis tetracycline resistance
RT plasmid, pCF10."
RL J. Biol. Chem. 263:14574-14578(1988).
CC -!- FUNCTION: CCF10 is involved in the conjugative transfer of the
CC hemolysin plasmid pCF10.
DR PIR; A30812; A30812.
KW Direct protein sequencing; Pheromone.
SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
Db 3 TL 4

RESULT 13
CHOX_ALCSP STANDARD; PRT; 7 AA.
ID CHOX_ALCSP
AC P16101;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Choline oxidase (EC 1.1.3.17) (Fragment).
OS Alcaligenes sp.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Alcaligenes.
OX NCBI_TaxID=512;
RN [1]
RP SEQUENCE.
RX MEDLINE=81006769; PubMed=6997283;
RA Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.;
RT "Identification and properties of the prosthetic group of choline
RT oxidase from Alcaligenes sp."
RL J. Biochem. 88:197-203(1980).
CC -!- CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2).
DR PIR; A15398; A15398.
KW Direct protein sequencing; Oxidoreductase.
FT NON TER 7
SQ SEQUENCE 7 AA; 839 MW; 7415B1E457644AC0 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SR 7 27.3%; Score 9; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 6 SR 7

QY 2 TLK 4
Db 2 TAK 4

Search completed: November 4, 2004, 07:09:40
Job time : 190 secs

RESULT 14
CIA_ENTFA STANDARD; PRT; 7 AA.
AC P11932;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sex pheromone CAM373 (Clumping-inducing agent) (CIA).
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=87005252; PubMed=3093276;
RA Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
RA White B.A., An F.Y., Clewell D.B., Suzuki A.;
RT "Isolation and structure of the Streptococcus faecalis sex pheromone,
RT CAM373.";
RL FEBS Lett. 206:69-72(1986).
CC -!- FUNCTION: CAM373 induces mating response of donor cells harboring
CC pAM373.
CC -!- MISCELLANEOUS: The N-terminus is possibly responsible for
CC specificity of pheromones to plasmids.
DR PIR; A25269; A25269.
KW Direct protein sequencing; Pheromone.
SQ SEQUENCE 7 AA; 734 MW; 75BDD72059C05DB0 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3
Db 3 FIL 5

RESULT 15
UC24_MAIZE STANDARD; PRT; 7 AA.
AC P80630;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 447)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program."
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.0, its MW is: 30.0 kDa.
DR Maize-2DPAGE; P80630; COLEOPTILE.
DR MaizeDB; 123956; -.
KW Direct protein sequencing.
FT NON_TER 1
FT NON_TER 7
SQ SEQUENCE 7 AA; 665 MW; 6DC1B5B33DC1B5D0 CRC64;

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OM protein - protein search, using sw model

Run on: November 4, 2004, 06:52:27 ; Search time 152 Seconds
(without alignments)
16.520 Million cell updates/sec

Title: US-09-712-819D-6
Perfect score: 33
Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 116873

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	23	69.7	7	2	AAY40736 S4 deriva
2	23	69.7	7	3	AAB30074 Scaffold
3	22	66.7	7	2	AAY40738 S4 deriva
4	22	66.7	7	3	AAB30076 Scaffold
5	21	63.6	7	2	AAY42013 Rheumatoid
6	20	60.6	7	2	AAR81848 Human afa
7	20	60.6	7	2	AAY41889 Rheumatoid
8	20	60.6	7	4	ABB55870 Vascular
9	20	60.6	7	4	ABB56283 Vascular
10	20	60.6	7	4	ABB55981 Vascular
11	20	60.6	7	4	AAY28602 DPI trypt
12	20	60.6	7	4	AAY24969 Schizoph
13	20	60.6	7	4	AAY26249 Depressio
14	20	60.6	7	4	AAY15313 Schizoph
15	20	60.6	7	4	ABB52190 Human API
16	20	60.6	7	4	ABB52355 Human API
17	20	60.6	7	5	ABG78901 Multiple
18	20	60.6	7	5	ABG78730 Multiple
19	20	60.6	7	6	ABP58010 Prostate
20	20	60.6	7	6	ABP57255 Breast ca
21	20	60.6	7	6	ABP57203 Breast ca
22	20	60.6	7	6	ABR59010 Alzheimer
23	20	60.6	7	6	ABR59042 Alzheimer
24	20	60.6	7	8	ADH35821 Vitamin D
25	20	60.6	7	8	ADH35827 Vitamin D

26	20	60.6	7	8	ADN31805 Human Alz
27	20	60.6	7	8	ADN32134 Human Alz
28	20	60.6	7	8	ADO78580 Schizoph
29	19	57.6	7	2	AAY40737 S4 deriva
30	19	57.6	7	3	AAB30075 Scaffold
31	19	57.6	7	7	ADB79629 Parapoxvi
32	19	57.6	7	8	ADP75041 Parapoxvi
33	18	54.5	7	5	ABP66518 Human RSV
34	18	54.5	7	5	ABR40481 Human sec
35	18	54.5	7	5	ABB81854 Staphyloc
36	18	54.5	7	6	ABU69381 Respirato
37	18	54.5	7	7	ADE35876 SYNAGIS a
38	18	54.5	7	7	ADE77927 Synthetic
39	18	54.5	7	8	ADI57038 RSV antib
40	17	51.5	6	2	AAW84431 HIV-1 nuc
41	17	51.5	6	5	AEE28110 Human imm
42	17	51.5	6	6	ABP95994 Microtetr
43	17	51.5	7	2	AAR07656 Ribonucle
44	17	51.5	7	2	AAR97970 Antigenic
45	17	51.5	7	2	AAW69269 Haemagglu

ALIGNMENTS

RESULT 1
AAY40736
ID AAY40736 standard; peptide; 7 AA.
XX
AC AAY40736;
XX
DT 01-DEC-1999 (first entry)
XX
DE S4 derivative #10, beta strand of scaffold protein structure.
XX
KW Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
KW tumour; chemotherapeutic agent.
XX
OS Synthetic.
XX
PN EP947582-A1.
XX
PD 06-OCT-1999.
XX
PF 31-MAR-1998; 98EP-00870065.
XX
PR 31-MAR-1998; 98EP-00870065.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Desmet J, Hufton S, Hoogenboom H, Sablon E;
XX
DR WPI; 1999-542958/46.
XX
PT New scaffold protein, useful for stabilizing antigens used as vaccines.
XX
PS Disclosure; Page 6; 105pp; English.
XX

Sequences AAY40727-Y40748 are functionally equivalent derivatives of the S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-Y40609) together form a single-chain scaffold protein which contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at least 6 beta-strands. The scaffold protein is constructed of beta strands S1-S6, and may also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to the next by hydrogen bonds, which generate a beta sandwich architecture. If the additional beta strands A1-A3 are included in the structure the scaffold is constructed of two beta sheets, with the structures A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each other via amino acid loops, where at least one of the loops binds to a receptor or antigen. The scaffold protein is used to stabilize antigens

CC or whole proteins such as receptors, or their fragments. It may be used
CC to bind two separate molecules. For example, one surface of the scaffold
CC may be bound to a protein which binds to a tumour antigen. This will
CC target the complex to tumour cells. Another surface may be bound to a
CC cytotoxic molecule or an autoimmune antibody which may then kill the
CC tumour cells. Therefore the scaffold protein may be used to target
CC chemotherapeutic agents to specific cells. It may also be used to
CC stabilize individual peptides in a peptide library and may be used in
CC diagnostic techniques, and to stabilize antigens used as vaccines
XX
SQ Sequence 7 AA;

Query Match 69.7%; Score 23; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKIS 6
||| ||
Db 2 FTLTIS 7

RESULT 2
AAB30074
ID AAB30074 standard; peptide; 7 AA.
XX
AC AAB30074;
XX
DT 09-FEB-2001 (first entry)
XX
DE Scaffold protein SCA S4 peptide SEQ ID NO: 135.
XX
KW Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
KW SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis;
KW diabetic retinopathy; atherosclerosis.
XX
OS Synthetic.
XX WO200060070-A1.
PN
XX 12-OCT-2000.
PD
XX 01-APR-1999; 99WO-EP002283.
PF
XX 01-APR-1999; 99WO-EP002283.
PR
XX (INNO-) INNOGENETICS NV.
PA
XX Desmet J, Hufton S, Hoogenboom H, Sablon E;
PI WPI; 2000-665002/64.
DR
XX Scaffold composed of single-chain polypeptide having beta sandwich
PT architecture carrying new and randomized peptide sequences useful as
PT supporting framework and carrying antigen- or receptor binding fragments.
XX
PS Disclosure; Page 15; 68pp; English.
XX
CC The present invention is concerned with producing scaffold proteins based
CC upon the human CTLA-4 SCA domain. These scaffold proteins can be used as
CC a scaffold to bind antigen- or receptor-binding fragments. These can be
CC used in the treatment of diseases such as cancer, atherosclerosis,
CC thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy.
CC Sequences AAB29930-B29939 were used in the production of the proteins of
CC the invention
XX
SQ Sequence 7 AA;

Query Match 69.7%; Score 23; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKIS 6
||| ||

Db 2 FTLTIS 7

RESULT 3
AAY40738
ID AAY40738 standard; peptide; 7 AA.
XX
AC AAY40738;
XX
DT 01-DEC-1999 (first entry)
XX
DE S4 derivative #12, beta strand of scaffold protein structure.
XX
KW Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
KW tumour; chemotherapeutic agent.
XX
OS Synthetic.
XX EP947582-A1.
PN
XX 06-OCT-1999.
PD
XX 31-MAR-1998; 98EP-00870065.
PF
XX 31-MAR-1998; 98EP-00870065.
PR
XX (INNO-) INNOGENETICS NV.
PA
XX Desmet J, Hufton S, Hoogenboom H, Sablon E;
PI WPI; 1999-542958/46.
DR
XX New scaffold protein, useful for stabilizing antigens used as vaccines.
PT
XX Disclosure; Page 6; 105pp; English.
PS
XX Sequences AAY40727-Y40748 are functionally equivalent derivatives of the
CC S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a
CC beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-
CC Y40609) together form a single-chain scaffold protein which contains at
CC least 1 disulfide bond, contains less than 10% alpha helix and contains
CC at least 6 beta-strands. The scaffold protein is constructed of beta
CC strands S1-S6, and may also include beta strands A1-A3, or any
CC functionally equivalent derivative of these sequences. The beta strands
CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to
CC the next by hydrogen bonds, which generate a beta sandwich architecture.
CC If the additional beta strands A1-A3 are included in the structure the
CC scaffold is constructed of two beta sheets, with the structures
CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each
CC other via amino acid loops, where at least one of the loops binds to a
CC receptor or antigen. The scaffold protein is used to stabilize antigens
CC or whole proteins such as receptors, or their fragments. It may be used
CC to bind two separate molecules. For example, one surface of the scaffold
CC may be bound to a protein which binds to a tumour antigen. This will
CC target the complex to tumour cells. Another surface may be bound to a
CC cytotoxic molecule or an autoimmune antibody which may then kill the
CC tumour cells. Therefore the scaffold protein may be used to target
CC chemotherapeutic agents to specific cells. It may also be used to
CC stabilize individual peptides in a peptide library and may be used in
CC diagnostic techniques, and to stabilize antigens used as vaccines
XX
SQ Sequence 7 AA;

Query Match 66.7%; Score 22; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKIS 6
||| ||
Db 2 FTLTIS 7

RESULT 4

AAB30076
ID AAB30076 standard; peptide; 7 AA.
XX
AC AAB30076;
XX
DT 09-FEB-2001 (first entry)
XX
DE Scaffold protein SCA S4 peptide SEQ ID NO: 137.
XX
DE Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
KW SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis;
KW diabetic retinopathy; atherosclerosis.
XX
OS Synthetic.
XX
PN WO200060070-A1.
XX
PD 12-OCT-2000.
XX
PF 01-APR-1999; 99WO-EP002283.
XX
PR 01-APR-1999; 99WO-EP002283.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Desmet J, Hufton S, Hoogenboom H, Sablon E;
XX WPI; 2000-665002/64.
XX
PT Scaffold composed of single-chain polypeptide having beta sandwich
PT architecture carrying new and randomized peptide sequences useful as
PT supporting framework and carrying antigen- or receptor binding fragments.
XX
PS Disclosure; Page 15; 68pp; English.
XX
CC The present invention is concerned with producing scaffold proteins based
CC upon the human CTLA-4 SCA domain. These scaffold proteins can be used as
CC a scaffold to bind antigen- or receptor-binding fragments. These can be
CC used in the treatment of diseases such as cancer, atherosclerosis,
CC thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy.
CC Sequences AAB29930-B29939 were used in the production of the proteins of
CC the invention
XX
SQ Sequence 7 AA;
Query Match 66.7%; Score 22; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 FTLKIS 6
Db 2 FTLTIS 7
RESULT 5
AAY42013
ID AAY42013 standard; peptide; 7 AA.
XX
AC AAY42013;
XX
DT 09-DEC-1999 (first entry)
XX
DE Rheumatoid arthritis diagnostic protein isoform peptide #164.
XX
KW Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;
KW rheumatoid arthritis diagnostic feature; ERPI; synovial fluid;
KW rheumatoid arthritis diagnostic protein isoform; screening;
KW expression reference protein isoform; prognosis.
XX
OS Homo sapiens.
XX
PN WO9947925-A2.
XX
PD 12-OCT-1995.
23-SEP-1999.
15-MAR-1999; 99WO-GB000763.
13-MAR-1998; 98GB-00005477.
(OXFO-) OXFORD GLYCOSCIENCES UK LTD.
Parekh RB, Patel TP, Townsend RR;
WPI; 1999-571871/48.
Diagnosis of human rheumatoid arthritis by two-dimensional
electrophoresis.
Disclosure; Page 21; 157pp; English.
A method has been developed for the diagnosis of human rheumatoid
arthritis (RA) using two-dimensional electrophoresis to generate a two-
dimensional array of features. The method can be used for screening,
diagnosis and prognosis of RA in a subject or for monitoring the effect
of an anti-RA drug or therapy administered to a subject. The method
comprises: (a) analysing a sample of serum or plasma and optionally
synovial fluid by two-dimensional electrophoresis, to generate a two-
dimensional array of features; (b) identifying at least one chosen
feature whose relative abundance correlates with the presence or absence
of RA; and (c) comparing the abundance of each chosen feature in the
sample with the abundance of that chosen feature in serum or plasma from
one or more persons without RA, where the relative abundance of the
chosen feature or features in the sample indicates the presence or
absence of RA in the subject. The method can also be used in clinical
studies for testing drugs for therapy of RA, for purification of RA-
diagnostic protein isoforms (RPIs), and for production of antibodies to
RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify
compounds that promote or inhibit their activity, which are then used as
RA drugs. Nucleic acid encoding RADFs can be used in gene therapy
protocols. AAY41844 to AAY42100 represent RPI peptides, AAY42101 to
AAY42103 represent expression reference protein isoform peptides and
AAZ25066 to AAZ25068 represent degenerate probes for RPIs, which are all
used in the exemplification of the present invention
Sequence 7 AA;
Query Match 63.6%; Score 21; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 TLKISR 7
Db 2 TLMISR 7
RESULT 6
AAR81848
ID AAR81848 standard; peptide; 7 AA.
XX
AC AAR81848;
XX
DT 16-MAY-1996 (first entry)
XX
DE Human afamin tryptic fragment FX20.
XX
KW Human; afamin; serum protein family; albumin; alpha-fetoprotein; plasma;
KW vitamin D binding protein; homology; post-translational processing;
KW chromatography; Primer; PCR; amplification; probe; rheumatoid arthritis;
KW ischaemia-reperfusion injury; ARPS; cardiopulmonary bypass; sepsis;
KW toxic plasma substance; inflammation.
XX
OS Homo sapiens.
XX
PN WO9527059-A1.
XX
PD 12-OCT-1995.

XX PF 31-MAR-1995; 95WO-US004075.
XX PR 31-MAR-1994; 94US-00222619.
XX (AMGE-) AMGEN INC.
PA (UYRQ) UNIV ROCKEFELLER.
XX Lichenstein HS, Lyons DE, Wurfel MM, Wright SD;
XX WPI; 1995-358634/46.
XX Human afamin or a variant and poly:nucleotide(s) encoding it - a human
PT serum protein with activities in common with other members of this
PT family.
XX Example 3; Page 45; 97pp; English.
XX Peptides AAR81847-54 are tryptic peptide fragments from human afamin
CC (AAR81845) novel member of the human serum protein family. The fragments
CC were used to design primers and probes (AAT00786-98) for the cloning of
CC the afamin gene (AAT00785) from human liver cDNA. Afamin is thought to
CC have similar properties to human albumin, alpha-foetoprotein and vitamin
CC D binding protein due to homology with these proteins. The gene encodes a
CC mature protein of 66576 daltons without post-translational processing
CC (ca. 87000 daltons with post-translational processing). The protein was
CC isolated from human plasma by a conventional chromatographic methods. The
CC protein can be used to ameliorate ischaemia-reperfusion injury,
CC rheumatoid arthritis, ARDS, cardiopulmonary bypass, sepsis, toxic plasma
CC substances released after inflammation, etc
XX Sequence 7 AA;
Query Match 60.6%; Score 20; DB 2; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 FTLKISR 7
Db 1 FTFEYSR 7
RESULT 7
AAY41889
ID AAY41889 standard; peptide; 7 AA.
XX
AC AAY41889;
XX
DT 09-DEC-1999 (first entry)
XX
DE Rheumatoid arthritis diagnostic protein isoform peptide #40.
XX
KW Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;
KW rheumatoid arthritis diagnostic feature; ERPI; synovial fluid;
KW rheumatoid arthritis diagnostic protein isoform; screening;
KW expression reference protein isoform; prognosis.
XX
OS Homo sapiens.
XX
XX WO9947925-A2.
PN
XX
PD 23-SEP-1999.
PD
XX
PF 15-MAR-1999; 99WO-GB000763.
PF
XX
PR 13-MAR-1998; 98GB-00005477.
PR
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Parekh RB, Patel TP, Townsend RR;
XX
XX WPI; 1999-571871/48.
DR
XX

PT Diagnosis of human rheumatoid arthritis by two-dimensional
PT electrophoresis.
XX
PS Disclosure; Page 18; 157pp; English.
XX
CC A method has been developed for the diagnosis of human rheumatoid
CC arthritis (RA) using two-dimensional electrophoresis to generate a two-
CC dimensional array of features. The method can be used for screening,
CC diagnosis and prognosis of RA in a subject or for monitoring the effect
CC of an anti-RA drug or therapy administered to a subject. The method
CC comprises: (a) analysing a sample of serum or plasma and optionally
CC synovial fluid by two-dimensional electrophoresis, to generate a two-
CC dimensional array of features; (b) identifying at least one chosen
CC feature whose relative abundance correlates with the presence or absence
CC of RA; and (c) comparing the abundance of each chosen feature in the
CC sample with the abundance of that chosen feature in serum or plasma from
CC one or more persons without RA, where the relative abundance of the
CC chosen feature or features in the sample indicates the presence or
CC absence of RA in the subject. The method can also be used in clinical
CC studies for testing drugs for therapy of RA, for purification of RA-
CC diagnostic protein isoforms (RPIs), and for production of antibodies to
CC RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify
CC compounds that promote or inhibit their activity, which are then used as
CC RA drugs. Nucleic acid encoding RADFs can be used in gene therapy
CC protocols. AAY41844 to AAY42100 represent RPI peptides, AAY42101 to
CC AAY42103 represent expression reference protein isoform peptides and
CC AAZ25066 to AAZ25068 represent degenerate probes for RPIs, which are all
CC used in the exemplification of the present invention
XX
SQ Sequence 7 AA;
Query Match 60.6%; Score 20; DB 2; Length 7;
Best Local Similarity 42.9%; Pred. No. 1.7e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 1 FTLKISR 7
Db 1 YTFELSR 7
RESULT 8
ABB55870
ID ABB55870 standard; peptide; 7 AA.
XX
AC ABB55870;
XX
DT 15-FEB-2002 (first entry)
XX
DE Vascular dementia-associated protein isoform (VPI) 70.
XX
XX Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
KW diagnosis; prognosis; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200169261-A2.
PN
XX
PD 20-SEP-2001.
PD
XX
XX 14-MAR-2001; 2001WO-GB001106.
PF
XX
PR 15-MAR-2000; 2000GB-00006285.
PR
PR 24-NOV-2000; 2000GB-00028734.
PR
PR 28-NOV-2000; 2000US-00724391.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
XX Herath HMAc, Parekh RB, Rohlff C;
XX
XX WPI; 2001-557937/62.
DR
XX
XX Screening, diagnosis or prognosis of vascular dementia (VD), useful for
PT determining stage of VD and monitoring the effect of VD therapy,
PT

PT comprises analyzing body fluid by 2-dimensional electrophoresis for
 PT features correlated with VD.
 XX
 PS Claim 6; Page 31; 151pp; English.
 XX
 CC The invention relates to screening, diagnosis or prognosis of Vascular
 CC Dementia (VD) in a subject comprising analysing body fluid from the
 CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
 CC features containing at least one chosen feature whose relative abundance
 CC correlates with the presence, absence, stage or severity of VD or
 CC predicts the onset or course of VD, especially detecting in a sample of
 CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
 CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
 CC specification. Detecting VD-associated features and VPI is useful for the
 CC screening, diagnosis or prognosis of VD, for determining the stage or
 CC severity of VD, for identifying a subject at risk of VD or for monitoring
 CC the effect of therapy administered to a subject having VD. Nucleic acids
 CC encoding a VPI or inhibiting the function of a VPI are useful for the
 CC treatment of VD and for gene therapy
 XX
 SQ Sequence 7 AA;

Query Match 60.6%; Score 20; DB 4; Length 7;
 Best Local Similarity 42.9%; Pred. No. 1.7e+06;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7
 :||:|
 Db 1 YTFELSR 7

RESULT 9
 ABB56283
 ID ABB56283 standard; peptide; 7 AA.
 XX
 AC ABB56283;
 XX
 DT 15-FEB-2002 (first entry)
 XX
 DE Vascular dementia-associated protein isoform (VPI) 483.
 XX
 KW Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
 KW diagnosis; prognosis; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200169261-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 14-MAR-2001; 2001WO-GB001106.
 XX
 PR 15-MAR-2000; 2000GB-00006285.
 PR 24-NOV-2000; 2000GB-00028734.
 PR 28-NOV-2000; 2000US-00724391.
 XX
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX
 PI Herath HMCAC, Parekh RB, Rohlf C;
 PI WPI; 2001-557937/62.
 DR
 XX
 PT Screening, diagnosis or prognosis of vascular dementia (VD), useful for
 PT determining stage of VD and monitoring the effect of VD therapy,
 PT comprises analyzing body fluid by 2-dimensional electrophoresis for
 PT features correlated with VD.
 XX
 PS Claim 6; Page 40; 151pp; English.
 XX
 CC The invention relates to screening, diagnosis or prognosis of Vascular
 CC Dementia (VD) in a subject comprising analysing body fluid from the
 CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
 CC features containing at least one chosen feature whose relative abundance

CC correlates with the presence, absence, stage or severity of VD or
 CC predicts the onset or course of VD, especially detecting in a sample of
 CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
 CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
 CC specification. Detecting VD-associated features and VPI is useful for the
 CC screening, diagnosis or prognosis of VD, for determining the stage or
 CC severity of VD, for identifying a subject at risk of VD or for monitoring
 CC the effect of therapy administered to a subject having VD. Nucleic acids
 CC encoding a VPI or inhibiting the function of a VPI are useful for the
 CC treatment of VD and for gene therapy
 XX
 SQ Sequence 7 AA;

Query Match 60.6%; Score 20; DB 4; Length 7;
 Best Local Similarity 42.9%; Pred. No. 1.7e+06;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7
 :||:|
 Db 1 YTFELSR 7

RESULT 10
 ABB55981
 ID ABB55981 standard; peptide; 7 AA.
 XX
 AC ABB55981;
 XX
 DT 15-FEB-2002 (first entry)
 XX
 DE Vascular dementia-associated protein isoform (VPI) 181.
 XX
 KW Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
 KW diagnosis; prognosis; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200169261-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 14-MAR-2001; 2001WO-GB001106.
 XX
 PR 15-MAR-2000; 2000GB-00006285.
 PR 24-NOV-2000; 2000GB-00028734.
 PR 28-NOV-2000; 2000US-00724391.
 XX
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX
 PI Herath HMCAC, Parekh RB, Rohlf C;
 PI WPI; 2001-557937/62.
 DR
 XX
 PT Screening, diagnosis or prognosis of vascular dementia (VD), useful for
 PT determining stage of VD and monitoring the effect of VD therapy,
 PT comprises analyzing body fluid by 2-dimensional electrophoresis for
 PT features correlated with VD.
 XX
 PS Claim 6; Page 33; 151pp; English.
 XX
 CC The invention relates to screening, diagnosis or prognosis of Vascular
 CC Dementia (VD) in a subject comprising analysing body fluid from the
 CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
 CC features containing at least one chosen feature whose relative abundance
 CC correlates with the presence, absence, stage or severity of VD or
 CC predicts the onset or course of VD, especially detecting in a sample of
 CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
 CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
 CC specification. Detecting VD-associated features and VPI is useful for the
 CC screening, diagnosis or prognosis of VD, for determining the stage or
 CC severity of VD, for identifying a subject at risk of VD or for monitoring
 CC the effect of therapy administered to a subject having VD. Nucleic acids
 CC encoding a VPI or inhibiting the function of a VPI are useful for the

KW CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;
 KW attention deficient disorder; schizoaffective disorder;
 KW unipolar affective disorder.
 XX Homo sapiens.
 OS
 XX WO200163294-A2.
 PN
 XX
 XX PD 30-AUG-2001.
 XX
 XX PF 23-FEB-2001; 2001WO-GB000791.
 XX
 XX PR 24-FEB-2000; 2000GB-00004412.
 PR 08-DEC-2000; 2000GB-00030050.
 PR 12-DEC-2000; 2000US-0254830P.
 XX
 XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX
 XX PI Herath HMC, Parekh RB, Rohlf C;
 XX WPI; 2001-582081/65.
 DR
 XX
 XX PT Preparation for diagnosing or treating bipolar affected disorder (BAD) or
 PT unipolar depression, or for screening for modulators, comprises a BAD-
 PT associated protein isoform.
 XX
 XX PS Claim 8; Page 34; 163pp; English.
 XX
 CC The invention relates to a preparation comprising an isolated Bipolar
 CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are
 CC used to screen, diagnose or prognosis of BAD or unipolar depression,
 CC determine the stage or severity of BAD or unipolar depression, identify a
 CC subject at risk of developing BAD or unipolar depression, or monitor the
 CC effect of therapy in a subject. They are also used to screen for or
 CC identify agents that interact with a DPI. These agents, antibodies
 CC against the DPIs, and nucleic acids encoding the DPIs are used to treat
 CC or prevent BAD or unipolar depression. Diseases that can be treated are
 CC attention deficient disorder, a schizoaffective disorder, a bipolar or a
 CC unipolar affective disorder. The DPIs are used in proteomics. The
 CC proteomic approach of using DPIs for screening, diagnosis or prognosis of
 CC BAD or unipolar depression overcomes the problems of using gene
 CC expression analysis, such as not being able to obtain central nervous
 CC system (CNS) tissue from a living patient under normal circumstances. The
 CC present sequence is a DIP decreased in the CSF (cerebro-spinal fluid) of
 CC subjects having BAD
 XX
 SQ Sequence 7 AA;
 Query Match 60.6%; Score 20; DB 4; Length 7;
 Best Local Similarity 42.9%; Pred. No. 1.7e+06;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FTLKISR 7
 Db :| :||
 1 YTFELSR 7
 RESULT 14
 AAU15313
 ID AAU15313 standard; peptide; 7 AA.
 XX
 AC AAU15313;
 XX
 XX DT 24-OCT-2001 (first entry)
 XX
 DE Schizophrenia-associated isoform peptide #198.
 XX
 KW Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;
 KW neurological disorder; neuropathy.
 XX
 OS Homo sapiens.
 XX
 PN WO200163293-A2.

XX 30-AUG-2001.
 PD
 XX 23-FEB-2001; 2001WO-GB000783.
 PF
 XX 24-FEB-2000; 2000GB-00004415.
 PR 28-DEC-2000; 2000US-00750395.
 PR
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PA
 XX Herath HMC, Parekh RB, Rohlf C;
 XX WPI; 2001-502868/55.
 DR
 XX
 XX PT Diagnosing and monitoring Schizophrenia by detecting the presence of
 PT Schizophrenia Associated Features and Schizophrenia Associated Protein
 PT Isoforms in samples of cerebrospinal fluid.
 XX
 XX PS Claim 6; Page 32; 160pp; English.
 XX
 CC The invention relates to methods and compositions for screening,
 CC diagnosis and prognosis of Schizophrenia. The method involves detecting
 CC the presence of Schizophrenia (SCH) Associated Features (SFs) and SCH
 CC Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis,
 CC immunoassay or hybridisation assay, for diagnosing and monitoring SCH,
 CC studying the effectiveness of treatments and for identifying potential
 CC therapeutic agents. The method is used for (1) screening or diagnosis of
 CC SCH and the relative abundance of at least 1 chosen feature correlates
 CC with the presence or absence of SCH; and (2) monitoring the effect of
 CC therapy administered to a subject with SCH and the relative abundance of
 CC at least 1 chosen feature which correlates with the severity of SCH. The
 CC expression and activity of the SPIs, SPIs and related molecules (e.g.
 CC secondary messengers) are studied to diagnose SCH, monitor the progress
 CC of the disorder and the effectiveness of treatment and as targets to
 CC identify and produce potential therapeutic agents for the treatment of
 CC SCH. The paucity of detectable neuroalgalic defects distinguishes
 CC neuropsychiatric disorders such as SCH from neurological disorders, where
 CC manifestations of anatomical and biochemical changes have been identified
 CC in many cases. Consequently the identification and characterisation of
 CC cellular and/or molecular causative defects and neuropathies are
 CC necessary for improved treatment of neuropsychiatric disorders. AAU1514-
 CC AAU15762 represent the amino acid sequences of schizophrenia-associated
 CC isoforms used in the method of the invention
 XX
 SQ Sequence 7 AA;
 Query Match 60.6%; Score 20; DB 4; Length 7;
 Best Local Similarity 42.9%; Pred. No. 1.7e+06;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FTLKISR 7
 Db :| :||
 1 YTFELSR 7
 RESULT 15
 ABB52190
 ID ABB52190 standard; peptide; 7 AA.
 XX
 AC ABB52190;
 XX
 XX DT 08-FEB-2002 (first entry)
 XX
 DE Human API-146 tryptic digest peptide #1.
 XX
 KW Human; neuroprotective; nootropic; gene therapy; vaccine;
 KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
 KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
 KW Expression Reference Protein Isoform; ERPI; proteolysis.
 XX
 OS Homo sapiens.
 XX
 PN WO200175454-A2.

XX
PD
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PF
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PR
PR
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PA
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PI
PI
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PS
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CC
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CC
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CC
CC
XX
SQ

11-OCT-2001.
03-APR-2001; 2001WO-US010908.
03-APR-2000; 2000US-0194504P.
28-NOV-2000; 2000US-0253647P.
(OXFO-) OXFORD GLYCOSCIENCES UK LTD.
(PFIZ) PFIZER INC.
Durham KL, Friedland DL, Herath HMA, Kimmel LH, Parekh RB;
Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;
Townsend RR, White F, Williams SA;
WPI; 2001-639384/73.
Screening for Alzheimer's disease in a mammal, by making two-dimensional
array of a feature whose relative abundance correlates with disease, and
comparing with abundance of the feature in samples of healthy persons.
Example; Page 30; 162pp; English.
The invention relates to methods for the screening, diagnosis and
prognosis of Alzheimer's disease. The methods involve the detection of
Alzheimer's Disease-Associated Features (AFs) and Alzheimer's Disease-
Associated Protein Isoforms (APIs) in cerebrospinal fluid, serum or
plasma. The abundance of the AFs and APIs is then normalised to an
Expression Reference Protein Isoform (ERPI) in order to determine whether
a patient is suffering from, or has a predisposition to, Alzheimer's
Disease. The relative abundance of the AFs and APIs correlates with the
severity of Alzheimer's Disease. The present sequence is a peptide
produced from an API by proteolysis
Sequence 7 AA;
Query Match 60.6%; Score 20; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 FTLKISR 7
|| : ||
Db 1 FTFEYSR 7
Search completed: November 4, 2004, 07:06:25
Job time : 154 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 07:09:49 ; Search time 140 Seconds
(without alignments)
17.661 Million cell updates/sec

Title: US-09-712-819D-6
Perfect score: 33
Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 353225886 residues

Total number of hits satisfying chosen parameters: 56374

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	20	60.6	7	9 US-09-791-378-198	Sequence 198, App
2	20	60.6	7	9 US-09-998-909-7	Sequence 7, Appli
3	20	60.6	7	9 US-09-826-290-205	Sequence 205, App
4	20	60.6	7	9 US-09-826-290-370	Sequence 370, App
5	20	60.6	7	10 US-09-791-393-145	Sequence 145, App
6	20	60.6	7	10 US-09-791-389-145	Sequence 145, App
7	20	60.6	7	11 US-09-791-377-198	Sequence 198, App
8	20	60.6	7	15 US-10-264-309-131	Sequence 131, App
9	20	60.6	7	15 US-10-264-309-460	Sequence 460, App
10	20	60.6	7	15 US-10-601-100-105	Sequence 105, App
11	20	60.6	7	17 US-10-700-340-52	Sequence 52, Appl
12	20	60.6	7	17 US-10-700-340-154	Sequence 154, App
13	18	54.5	7	9 US-09-996-288-164	Sequence 164, App

14	18	54.5	7	10	US-09-996-265-164	Sequence 164, App
15	18	54.5	7	14	US-10-162-497-78	Sequence 78, Appl
16	18	54.5	7	15	US-10-461-863-164	Sequence 164, App
17	17	51.5	6	14	US-10-105-930-39	Sequence 39, Appl
18	17	51.5	6	14	US-10-043-539-30	Sequence 30, Appl
19	17	51.5	6	14	US-10-020-354-101	Sequence 101, App
20	17	51.5	7	9	US-09-996-288-135	Sequence 135, App
21	17	51.5	7	10	US-09-996-265-135	Sequence 135, App
22	17	51.5	7	13	US-10-044-034-13	Sequence 13, Appl
23	17	51.5	7	15	US-10-461-863-135	Sequence 135, App
24	16	48.5	6	9	US-09-727-963A-88	Sequence 88, Appl
25	16	48.5	6	14	US-10-211-994-23	Sequence 23, Appl
26	16	48.5	6	14	US-10-020-354-87	Sequence 87, Appl
27	16	48.5	7	9	US-09-989-789-396	Sequence 396, App
28	16	48.5	7	9	US-09-989-789-1971	Sequence 1971, Ap
29	16	48.5	7	9	US-09-989-789-3503	Sequence 3503, Ap
30	16	48.5	7	9	US-09-989-789-3542	Sequence 3542, Ap
31	16	48.5	7	9	US-09-989-789-3544	Sequence 3544, Ap
32	16	48.5	7	9	US-09-796-848A-20	Sequence 20, Appl
33	16	48.5	7	9	US-09-844-508-43	Sequence 43, Appl
34	16	48.5	7	9	US-09-808-387-44	Sequence 44, Appl
35	16	48.5	7	9	US-09-996-288-35	Sequence 35, Appl
36	16	48.5	7	9	US-09-996-288-96	Sequence 96, Appl
37	16	48.5	7	9	US-09-996-288-131	Sequence 131, App
38	16	48.5	7	10	US-09-990-186-396	Sequence 396, App
39	16	48.5	7	10	US-09-990-186-1971	Sequence 1971, Ap
40	16	48.5	7	10	US-09-990-186-3503	Sequence 3503, Ap
41	16	48.5	7	10	US-09-990-186-3542	Sequence 3542, Ap
42	16	48.5	7	10	US-09-990-186-3544	Sequence 3544, Ap
43	16	48.5	7	10	US-09-996-265-35	Sequence 35, Appl
44	16	48.5	7	10	US-09-996-265-96	Sequence 96, Appl
45	16	48.5	7	10	US-09-996-265-131	Sequence 131, App

ALIGNMENTS

RESULT 1
US-09-791-378-198
; Sequence 198, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791,378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 198
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-198

Query Match 60.6%; Score 20; DB 9; Length 7;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
:|:|:
Db 1 YTFELSR 7

RESULT 2
US-09-998-909-7
; Sequence 7, Application US/09998909
; Patent No. US20020164664A1
; GENERAL INFORMATION:
; APPLICANT: Hlavaty, John

; APPLICANT: Briggman, Joseph
; TITLE OF INVENTION: Detection and Treatment of Prostate Cancer
; FILE REFERENCE: MTP-027
; CURRENT APPLICATION NUMBER: US/09/998,909
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/250,284
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-998-909-7

Query Match 60.6%; Score 20; DB 9; Length 7;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
:|:|
Db 1 YTFELSR 7

RESULT 3
US-09-826-290-205
; Sequence 205, Application US/09826290
; Patent No. US20020164668A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L.Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlff, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 205
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-205

Query Match 60.6%; Score 20; DB 9; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
||:|
Db 1 FTFEYSR 7

RESULT 4
US-09-826-290-370
; Sequence 370, Application US/09826290
; Patent No. US20020164668A1

; GENERAL INFORMATION:
; APPLICANT: Duzham, L.Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlff, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 370
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-370

Query Match 60.6%; Score 20; DB 9; Length 7;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
:|:|
Db 1 YTFELSR 7

RESULT 5
US-09-791-393-145
; Sequence 145, Application US/09791393
; Publication No. US20030032200A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlff, Christian
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-393-145

Query Match 60.6%; Score 20; DB 10; Length 7;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7
:|:|
Db 1 YTFELSR 7

RESULT 6

US-09-791-389-145
; Sequence 145, Application US/09791389
; Publication No. US20030032773A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; APPLICANT: Terrett, Jonathan Alexander
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/791,389
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GB 0004412.3
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GB 0030050.9
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/254,830
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-389-145

Query Match 60.6%; Score 20; DB 10; Length 7;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7
:|:|
Db 1 YTFELSR 7

RESULT 7

US-09-791-377-198
; Sequence 198, Application US/09791377
; Publication No. US20040110938A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-060-999
; CURRENT APPLICATION NUMBER: US/09/791,377
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 198
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-377-198

Query Match 60.6%; Score 20; DB 11; Length 7;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7
:|:|
Db 1 YTFELSR 7

RESULT 8

US-10-264-309-131
; Sequence 131, Application US/10264309
; Publication No. US20040022794A1
; GENERAL INFORMATION:
; APPLICANT: DURHAM, L. KATHRYN
; APPLICANT: FRIEDMAN, DAVID L.
; APPLICANT: HERATH, HERATH
; APPLICANT: KIMMEL, LIDA H.
; APPLICANT: PAREKH, RAJESH B.
; APPLICANT: POTTER, DAVID M.
; APPLICANT: ROHLFF, CHRISTIAN
; APPLICANT: SILBER, B. MICHAEL
; APPLICANT: SNYDER, PETER J.
; APPLICANT: SOARES, HOLLY D.
; APPLICANT: STIGER, THOMAS R.
; APPLICANT: SUNDERLAND, P. TREY
; APPLICANT: TOWNSEND, ROBERT R.
; APPLICANT: WHITE, W. FROST
; APPLICANT: WILLIAMS, STEPHEN A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
; TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
; FILE REFERENCE: POA-002.01
; CURRENT APPLICATION NUMBER: US/10/264,309
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: 60/326,708
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 131
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-309-131

Query Match 60.6%; Score 20; DB 15; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTLKISR 7
:|:|
Db 1 FTPEYSR 7

RESULT 9

US-10-264-309-460
; Sequence 460, Application US/10264309
; Publication No. US20040022794A1
; GENERAL INFORMATION:
; APPLICANT: DURHAM, L. KATHRYN
; APPLICANT: FRIEDMAN, DAVID L.
; APPLICANT: HERATH, HERATH
; APPLICANT: KIMMEL, LIDA H.
; APPLICANT: PAREKH, RAJESH B.
; APPLICANT: POTTER, DAVID M.
; APPLICANT: ROHLFF, CHRISTIAN
; APPLICANT: SILBER, B. MICHAEL
; APPLICANT: SNYDER, PETER J.
; APPLICANT: SOARES, HOLLY D.
; APPLICANT: STIGER, THOMAS R.
; APPLICANT: SUNDERLAND, P. TREY
; APPLICANT: TOWNSEND, ROBERT R.
; APPLICANT: WHITE, W. FROST
; APPLICANT: WILLIAMS, STEPHEN A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
; TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
; FILE REFERENCE: POA-002.01
; CURRENT APPLICATION NUMBER: US/10/264,309
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: 60/326,708
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 491

; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 460
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-309-460

Query Match 60.6%; Score 20; DB 15; Length 7;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
:|:|
Db 1 YTFELSR 7

RESULT 10
US-10-601-100-105
; Sequence 105, Application US/10601100
; Publication No. US20040072261A1
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: Method for the Diagnosis and Differential Diagnosis of
; TITLE OF INVENTION: Neurological Diseases
; FILE REFERENCE: 11362.0038.NPUS01
; CURRENT APPLICATION NUMBER: US/10/601,100
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: EP 02447121.1
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/396,437
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 105
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-601-100-105

Query Match 60.6%; Score 20; DB 15; Length 7;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
:|:|
Db 1 YTFELSR 7

RESULT 11
US-10-700-340-52
; Sequence 52, Application US/10700340
; Publication No. US20040203023A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF BREA
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 2543-1-032
; CURRENT APPLICATION NUMBER: US/10/700,340
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: PCT/GB02/02022
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: GB0110790.3
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: GB0118385.4
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: GB0119791.2
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB0120045.0
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: GB0128062.7
; PRIOR FILING DATE: 2001-11-22
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 52
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-700-340-52

Query Match 60.6%; Score 20; DB 17; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
:|:|
Db 1 YTFEYSR 7

RESULT 12
US-10-700-340-154
; Sequence 154, Application US/10700340
; Publication No. US20040203023A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF BREA
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 2543-1-032
; CURRENT APPLICATION NUMBER: US/10/700,340
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: PCT/GB02/02022
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: GB0110790.3
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: GB0118385.4
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: GB0119791.2
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB0120045.0
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: GB0128062.7
; PRIOR FILING DATE: 2001-11-22
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 154
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-700-340-154

Query Match 60.6%; Score 20; DB 17; Length 7;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
:|:|
Db 1 YTFELSR 7

RESULT 13
US-09-996-288-164
; Sequence 164, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylax
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 164
; LENGTH: 7
; TYPE: PRT


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; ORGANISM: Homo sapiens
US-09-996-288-164

Query Match      54.5%; Score 18; DB 9; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 TLKIS 6
      |:|:|
Db      2 TMKLS 6

RESULT 14
US-09-996-265-164
; Sequence 164, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 164
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-164

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```

Query Match      54.5%; Score 18; DB 10; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 TLKIS 6
      |:|:|
Db      2 TMKLS 6

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RESULT 15
US-10-162-497-78
; Sequence 78, Application US/10162497
; Publication No. US20030158398A1
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; APPLICANT: Freimer, N.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/10/162,497
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US/09/657,474
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 09/268,992
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/236,134
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/106,056
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/088,312
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/078,044
; PRIOR FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-497-78

```

```

Query Match      54.5%; Score 18; DB 14; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FTLKIS 6
      |:|:|
Db      2 YTMKYS 7

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Search completed: November 4, 2004, 07:21:29
Job time : 141 secs

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OM protein - protein search, using sw model

Run on: November 4, 2004, 06:45:39 ; Search time 38 Seconds
(without alignments)
12.216 Million cell updates/sec

Title: US-09-712-819D-6
Perfect score: 33
Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	33	100.0	32	1	US-08-477-877B-33	Sequence 33, Appl
2	33	100.0	32	1	US-07-977-696C-71	Sequence 71, Appl
3	33	100.0	32	1	US-08-129-930B-71	Sequence 71, Appl
4	33	100.0	32	2	US-08-472-281A-33	Sequence 33, Appl
5	33	100.0	32	2	US-08-477-989B-33	Sequence 33, Appl
6	33	100.0	32	3	US-08-976-288A-71	Sequence 71, Appl
7	33	100.0	32	4	US-09-563-222C-80	Sequence 80, Appl
8	33	100.0	32	4	US-09-563-222C-114	Sequence 114, App
9	33	100.0	81	1	US-08-497-312-19	Sequence 19, Appl
10	33	100.0	81	4	US-09-254-180C-154	Sequence 154, App
11	33	100.0	81	4	US-09-254-180C-155	Sequence 155, App
12	33	100.0	81	4	US-09-254-180C-156	Sequence 156, App
13	33	100.0	81	4	US-09-254-180C-157	Sequence 157, App
14	33	100.0	81	4	US-09-254-180C-158	Sequence 158, App
15	33	100.0	81	4	US-09-254-180C-159	Sequence 159, App
16	33	100.0	100	4	US-09-472-087-113	Sequence 113, App
17	33	100.0	100	4	US-09-472-087-115	Sequence 115, App
18	33	100.0	100	4	US-09-840-459-21	Sequence 21, Appl
19	33	100.0	100	4	US-09-840-459-22	Sequence 22, Appl
20	33	100.0	100	4	US-09-840-459-23	Sequence 23, Appl
21	33	100.0	100	4	US-09-840-459-24	Sequence 24, Appl
22	33	100.0	100	4	US-09-840-459-25	Sequence 25, Appl
23	33	100.0	100	4	US-09-840-459-26	Sequence 26, Appl
24	33	100.0	100	4	US-09-840-459-27	Sequence 27, Appl
25	33	100.0	100	4	US-09-840-459-28	Sequence 28, Appl
26	33	100.0	100	4	US-09-840-459-29	Sequence 29, Appl
27	33	100.0	100	4	US-09-840-459-30	Sequence 30, Appl

28	33	100.0	100	4	US-09-497-625A-21	Sequence 21, Appl
29	33	100.0	100	4	US-09-497-625A-22	Sequence 22, Appl
30	33	100.0	100	4	US-09-497-625A-23	Sequence 23, Appl
31	33	100.0	100	4	US-09-497-625A-24	Sequence 24, Appl
32	33	100.0	100	4	US-09-497-625A-25	Sequence 25, Appl
33	33	100.0	100	4	US-09-497-625A-26	Sequence 26, Appl
34	33	100.0	100	4	US-09-497-625A-27	Sequence 27, Appl
35	33	100.0	100	4	US-09-497-625A-28	Sequence 28, Appl
36	33	100.0	100	4	US-09-497-625A-29	Sequence 29, Appl
37	33	100.0	100	4	US-09-497-625A-30	Sequence 30, Appl
38	33	100.0	104	3	US-08-881-037-37	Sequence 37, Appl
39	33	100.0	108	1	US-08-488-113B-151	Sequence 151, App
40	33	100.0	108	1	US-08-477-484B-151	Sequence 151, App
41	33	100.0	108	1	US-08-107-669D-15	Sequence 15, Appl
42	33	100.0	108	1	US-08-472-788A-15	Sequence 15, Appl
43	33	100.0	108	2	US-08-477-531B-15	Sequence 15, Appl
44	33	100.0	108	2	US-08-646-360-151	Sequence 151, App
45	33	100.0	108	2	US-08-082-842A-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-477-877B-33
; Sequence 33, Application US/08477877B
; Patent No. 5730979
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activ
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,877B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-146
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-08-477-877B-33

Query Match

100.0%; Score 33; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.6; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 2

US-07-977-696C-71
; Sequence 71, Application US/07977696C
; Patent No. 5792852
; GENERAL INFORMATION:
; APPLICANT: do Couto, Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Specificity
; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
; TITLE OF INVENTION: and Therapeutic Methods.
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,696C
; FILING DATE: 11-16-92
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 748-6868
; TELEFAX: (510) 748-6688
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-977-696C-71

Query Match 100.0%; Score 33; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 3

US-08-129-930B-71
; Sequence 71, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and

; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. AMZEL & ASSOC.
; STREET: 2055 No. 5804187th Broadway, Suite 201
; CITY: Walnut Creek
; STATE: California
; COUNTRY: USA
; ZIP: 94596
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,930B
; FILING DATE: September 30, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: CRFCC-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 521-1333
; TELEFAX: (510) 521-3541
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-129-930B-71

Query Match 100.0%; Score 33; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 4

US-08-472-281A-33
; Sequence 33, Application US/08472281A
; Patent No. 5817311
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activity
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,281A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995

/ APPLICATION NUMBER: 08/119,032
/ FILING DATE: 09-SEP-1993
/ APPLICATION NUMBER: 08/027,008
/ FILING DATE: 05-MAR-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Olstein, Elliot M.
/ REGISTRATION NUMBER: 24,025
/ REFERENCE/DOCKET NUMBER: 61750-142
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-994-1700
/ TELEFAX: 201-994-1744
/ INFORMATION FOR SEQ ID NO: 33:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 32 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: polypeptide
US-08-472-281A-33

Query Match 100.0%; Score 33; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 5

US-08-477-989B-33
/ Sequence 33, Application US/08477989B
/ Patent No. 5951983

GENERAL INFORMATION:

/ APPLICANT: Bazin, Herv
/ APPLICANT: Latinne, Dominique
/ APPLICANT: Kaplan, Ruth
/ APPLICANT: Kieber-Emmons, Thomas
/ APPLICANT: Postema, Christina E.
/ APPLICANT: White-Scharf, Mary
/ TITLE OF INVENTION: LO-CD2a Antibody and Uses
/ TITLE OF INVENTION: Thereof for Inhibiting
/ TITLE OF INVENTION: T-Cell Activation and
/ TITLE OF INVENTION: Proliferation
/ NUMBER OF SEQUENCES: 96
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
/ ADDRESSEE: Cecchi, Stewart & Olstein
/ STREET: 6 Becker Farm Road
/ CITY: Roseland
/ STATE: New Jersey
/ COUNTRY: U.S.A.
/ ZIP: 07068

COMPUTER READABLE FORM:

/ MEDIUM TYPE: 3.5 inch diskette
/ COMPUTER: IBM PS/2
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: WordPerfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/477,989B
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/407,009
/ FILING DATE: 29-MAR-1995
/ APPLICATION NUMBER: 08/119,032
/ FILING DATE: 09-SEP-1993
/ APPLICATION NUMBER: 08/027,008
/ FILING DATE: 05-MAR-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Olstein, Elliot M.
/ REGISTRATION NUMBER: 24,025
/ REFERENCE/DOCKET NUMBER: 61750-147

/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-994-1700
/ TELEFAX: 201-994-1744
/ INFORMATION FOR SEQ ID NO: 33:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 32 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: polypeptide
US-08-477-989B-33

Query Match 100.0%; Score 33; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 6

US-08-976-288A-71
/ Sequence 71, Application US/08976288A
/ Patent No. 6315997

GENERAL INFORMATION:

/ APPLICANT: do Couto Dr., Fernando J.R.
/ APPLICANT: Ceriani Dr., Roberto L.
/ APPLICANT: Peterson Dr., Jerry A.
/ APPLICANT: Padlan Dr., Eduardo A.
/ TITLE OF INVENTION: Analogue Peptides With Broad
/ TITLE OF INVENTION: Carcinoma Specificity, and Kit and
/ TITLE OF INVENTION: Diagnostic Vaccination and
/ TITLE OF INVENTION: Therapeutic Methods
/ NUMBER OF SEQUENCES: 96
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pretty, Schroeder & Poplawski
/ STREET: 444 South Flower St., 19th Floor
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: USA
/ ZIP: 90071

COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/976,288A
/ FILING DATE: No. 6315997ember 21, 1997
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/129,930
/ FILING DATE: September 30, 1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/977,696
/ FILING DATE: No. 6315997ember 16, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Viviana Amzel Ph.D.
/ REGISTRATION NUMBER: 30,930
/ REFERENCE/DOCKET NUMBER: P6639938
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 622-7700
/ TELEFAX: (213) 489-4210
/ TELEX: n.a.
/ INFORMATION FOR SEQ ID NO: 71:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 32 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-976-288A-71

Query Match 100.0%; Score 33; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 7

US-09-563-222C-80
; Sequence 80, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-563-222C-80

Query Match 100.0%; Score 33; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 8

US-09-563-222C-114
; Sequence 114, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 114
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222C-114

Query Match 100.0%; Score 33; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 9

US-08-497-312-19
; Sequence 19, Application US/08497312
; Patent No. 5712120
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Method for obtaining modified
; TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine
; TITLE OF INVENTION: antibody variable domains, compositions containing them.
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR
; STREET: 215 Y 15, ATABEY PLAYA
; CITY: HAVANA
; STATE:
; COUNTRY: CUBA
; ZIP: 11600
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/497,312
; FILING DATE: 30-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CU 80/94
; FILING DATE: 30-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BOND, LAURENCE B.
; REGISTRATION NUMBER: 30,549
; REFERENCE/DOCKET NUMBER: 2629US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 801/532-1922
; TELEFAX: 801/531-9168
; TELEX: 388961 LPM04UT
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 81 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-497-312-19

Query Match 100.0%; Score 33; DB 1; Length 81;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 53 FTLKISR 59

RESULT 10

US-09-254-180C-154
; Sequence 154, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, KO
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand
; TITLE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand
; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254,180C
; CURRENT FILING DATE: 1999-04-15

; PRIOR APPLICATION NUMBER: PCT/JP97/02983
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: 271546/1996
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 231472/1996
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 154
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-180C-154

Query Match 100.0%; Score 33; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||
Db 53 FTLKISR 59

RESULT 11

US-09-254-180C-155
; Sequence 155, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, Ko
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi

; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
; TITLE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand

; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254,180C
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/JP97/02983
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: 271546/1996
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 231472/1996
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 155
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-180C-155

Query Match 100.0%; Score 33; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||
Db 53 FTLKISR 59

RESULT 12

US-09-254-180C-156
; Sequence 156, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, Ko
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi

; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
; TITLE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand
; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254,180C
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/JP97/02983
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: 271546/1996
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 231472/1996
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-09-254-180C-156

Query Match 100.0%; Score 33; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||
Db 53 FTLKISR 59

RESULT 13

US-09-254-180C-157
; Sequence 157, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, Ko
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi

; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
; TITLE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand

; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254,180C
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/JP97/02983
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: 271546/1996
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 231472/1996
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 157
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-09-254-180C-157

Query Match 100.0%; Score 33; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||
Db 53 FTLKISR 59

RESULT 14

US-09-254-180C-158

; Sequence 158, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, Ko
; APPLICANT: EDADA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
; TITLE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand
; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254,180C
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/JP97/02983
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: 271546/1996
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 231472/1996
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 158
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-09-254-180C-158

Query Match 100.0%; Score 33; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 53 FTLKISR 59

RESULT 15
US-09-254-180C-159
; Sequence 159, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, Ko
; APPLICANT: EDADA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
; TITLE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand
; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254,180C
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/JP97/02983
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: 271546/1996
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 231472/1996
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 159
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-09-254-180C-159

Query Match 100.0%; Score 33; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 4;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
Db 53 FTLKISR 59
Search completed: November 4, 2004, 06:53:08
Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 06:45:39 ; Search time 38 Seconds
(without alignments)
17.724 Million cell updates/sec

Title: US-09-712-819D-6
Perfect score: 33
Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	33	100.0	54	2	S34093	Ig kappa chain V r
2	33	100.0	71	2	H30538	Ig kappa chain V r
3	33	100.0	72	2	S40358	Ig kappa chain - h
4	33	100.0	75	2	S40337	Ig kappa chain V-J
5	33	100.0	83	2	S24211	Ig kappa chain V r
6	33	100.0	83	2	S34095	Ig kappa chain V r
7	33	100.0	87	2	S34091	Ig kappa chain V r
8	33	100.0	87	2	S34094	Ig kappa chain V r
9	33	100.0	89	2	B25155	Ig kappa chain V r
10	33	100.0	91	2	S42186	Ig kappa chain V r
11	33	100.0	91	2	S25463	Ig kappa chain V r
12	33	100.0	93	2	PH1039	Ig light chain V r
13	33	100.0	94	2	PL0258	Ig kappa chain V r
14	33	100.0	96	2	S40320	Ig kappa chain - h
15	33	100.0	99	2	E28833	Ig heavy chain V r
16	33	100.0	99	2	S24504	Ig kappa chain V r
17	33	100.0	99	2	S24501	Ig kappa chain V r
18	33	100.0	100	2	S45440	Ig kappa chain V r
19	33	100.0	100	2	S24681	Ig kappa chain V r
20	33	100.0	100	2	S26334	Ig kappa chain - h
21	33	100.0	101	2	C34153	Ig light chain V r
22	33	100.0	101	2	A33730	Ig kappa chain V-I
23	33	100.0	101	2	PH1057	Ig kappa chain V r
24	33	100.0	102	2	S14590	Ig light chain V r
25	33	100.0	102	2	S14591	Ig kappa chain V r
26	33	100.0	102	2	S14594	Ig kappa chain V r
27	33	100.0	102	2	S14592	Ig kappa chain V r
28	33	100.0	102	2	S14593	Ig kappa chain V r
29	33	100.0	102	2	PH1035	Ig light chain V r

30	33	100.0	102	2	E28195	Ig kappa chain V r
31	33	100.0	102	2	PH1044	Ig light chain V r
32	33	100.0	103	2	PH1099	Ig light chain V r
33	33	100.0	103	2	PH1056	Ig light chain V r
34	33	100.0	103	2	PH1100	Ig light chain V r
35	33	100.0	103	2	PH1041	Ig light chain V r
36	33	100.0	103	2	PH1098	Ig light chain V r
37	33	100.0	103	2	PH1040	Ig light chain V r
38	33	100.0	103	2	PH1045	Ig light chain V r
39	33	100.0	103	2	PH1042	Ig light chain V r
40	33	100.0	103	2	PH1031	Ig light chain V r
41	33	100.0	103	2	PH1034	Ig light chain V r
42	33	100.0	103	2	PH1038	Ig light chain V r
43	33	100.0	103	2	PH1030	Ig light chain V r
44	33	100.0	103	2	PH1043	Ig light chain V r
45	33	100.0	103	2	PH1055	Ig light chain V r

ALIGNMENTS

RESULT 1

S34093
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 07-May-1999
C;Accession: S34093
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34093
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-54 <WAG>
A;Cross-references: EMBL:X67177
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 FTLKISR 7
DB	43 FTLKISR 49

RESULT 2

H30538
Ig kappa chain V region (174.3F4) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 09-May-1997
C;Accession: H30538
R;Clafilin, J.L.; Berry, J.
J. Immunol. 141, 4012-4019, 1988
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneumoniae
A;Reference number: A30534; MUID:89035545; PMID:3141511
A;Accession: H30538
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-71 <CLA>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 FTLKISR 7
DB	35 FTLKISR 41

RESULT 3

S40358
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C;Accession: S40358
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40358
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-72 <KLE>
A;Cross-references: EMBL:X72468; NID:g441404; PIDN:CAA51136.1; PID:g441405
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||
Db 28 FTLKISR 34

RESULT 4

S40337
Ig kappa chain V-J-C region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C;Accession: S40337
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40337
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-75 <KLE>
A;Cross-references: EMBL:X72447; NID:g441362; PIDN:CAA51115.1; PID:g441363
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||
Db 30 FTLKISR 36

RESULT 5

S24211
Ig kappa chain V region (V3a) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S24211
R;Pargent, W.; Meindl, A.; Thiebe, R.; Mitzel, S.; Zachau, H.G.
Eur. J. Immunol. 21, 1821-1827, 1991
A;Title: The human immunoglobulin kappa locus. Characterization of the duplicated O region
A;Reference number: S24205; MUID:91330953; PMID:1907917
A;Accession: S24211
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-83 <PAR>
A;Cross-references: EMBL:X59317; NID:g33270; PIDN:CAA42004.1; PID:g33271
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||
Db 59 FTLKISR 65

RESULT 6

S34095
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S34095
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34095
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-83 <WAG>
A;Cross-references: UNIPROT:Q8TCD0; UNIPROT:Q9UL80; EMBL:X67179
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-80/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||
Db 61 FTLKISR 67

RESULT 7

S34091
Ig kappa chain V region (patient 19 and 20) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Accession: S34091; S34092
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34091
A;Molecule type: DNA
A;Residues: 1-87 <WAG>
A;Cross-references: UNIPROT:Q8NEK0; EMBL:X67175
A;Experimental source: patient 19
A;Accession: S34092
A;Molecule type: DNA
A;Residues: 1-87 <WAW>
A;Cross-references: EMBL:X67176
A;Experimental source: patient 20
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;3-82/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||
Db 63 FTLKISR 69

RESULT 8

S34094

Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S34094
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34094
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-87 <WAG>
A;Cross-references: UNIPROT:Q9UL80; EMBL:X67178
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;3-82/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
|||||
Db 63 FTLKISR 69

RESULT 9
B25155
Ig kappa chain V region (SM1.5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 02-Jun-1988 #text_change 16-Aug-1996
C;Accession: B25155
R;Robbins, P.F.; Rosen, E.M.; Haba, S.; Nisonoff, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 1050-1054, 1986
A;Title: Relationship of V(H) and V(L) genes encoding three idiotypic families of anti-p
A;Reference number: A94083; MUID:86149212; PMID:3081888
A;Accession: B25155
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-89 <ROB>
C;Comment: This chain is expressed in an IgM with anti-arsenate activity.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
|||||
Db 54 FTLKISR 60

RESULT 10
S42186
Ig kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S42186; S42195
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A;Reference number: S42176; MUID:94009207; PMID:7691608
A;Accession: S42186
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <MOJ>
A;Cross-references: EMBL:Z25442; NID:G407830; PIDN:CAA80929.1; PID:G407831
A;Note: the authors translated the codon GTT for residue 81 as Thr, TGG for residue 85 a
A;Accession: S42195
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <MO2>

A;Cross-references: EMBL:Z25460; NID:G407848; PIDN:CAA80947.1; PID:G407849
A;Note: the authors translated the codon GTT for residue 81 as Thr, TGG for residue 85
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-86/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
|||||
Db 67 FTLKISR 73

RESULT 11
S25463
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S25463
R;Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
submitted to the EMBL Data Library, July 1992
A;Description: Structure and binding properties of monoclonal antibodies to core histon
A;Reference number: S25174
A;Accession: S25463
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-91 <MON>

Query Match 100.0%; Score 33; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
|||||
Db 76 FTLKISR 82

RESULT 12
PH1039
Ig light chain V region (clone 165.27) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: PH1039
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1039
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-93 <TIL>
A;Cross-references: UNIPROT:Q99M37
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
|||||
Db 67 FTLKISR 73

RESULT 13
PL0258
Ig kappa chain V region (anti-DNA, 1E81VK) - mouse (fragment)

F;16-95/Domain: immunoglobulin homology <IMM>

Query Match	100.0%;	Score 33;	DB 2;	Length 99;
Best Local Similarity	100.0%;	Pred. No. 0.92;		
Matches	7;	Conservative	0;	Mismatches 0;
		Indels	0;	Gaps 0;

Qy 1 FTLKISR 7
| | | | |
Db 76 FTLKISR 82

Search completed: November 4, 2004, 06:52:23
Job time : 39 secs

C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C;Accession: PL0258
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0258
A;Molecule type: mRNA
A;Residues: 1-94 <SHL>
A;Cross-references: UNIPROT:Q9JL82
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-6/Region: framework 1
F;7-22/Region: complementarity-determining 1
F;23-37/Region: framework 2
F;38-44/Region: complementarity-determining 2
F;45-76/Region: framework 3
F;77-85/Region: complementarity-determining 3
F;86-94/Region: framework 4

Query Match	100.0%;	Score 33;	DB 2;	Length 94;
Best Local Similarity	100.0%;	Pred. No. 0.87;		
Matches	7;	Conservative	0;	Mismatches 0;
		Indels	0;	Gaps 0;

Qy 1 FTLKISR 7
| | | | |
Db 59 FTLKISR 65

RESULT 14
S40320
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C;Accession: S40320
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40320
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-96 <KLE>
A;Cross-references: EMBL:X72430; NID:g441328; PIDN:CAA51098.1; PID:g441329
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match	100.0%;	Score 33;	DB 2;	Length 96;
Best Local Similarity	100.0%;	Pred. No. 0.89;		
Matches	7;	Conservative	0;	Mismatches 0;
		Indels	0;	Gaps 0;

Qy 1 FTLKISR 7
| | | | |
Db 59 FTLKISR 65

RESULT 15
E28833
Ig heavy chain V region (HP22.111.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: E28833
R;Corbet, S.; Harn, M.; Roth, C.; Theze, J.; Fougereau, M.; Schiff, C.
J. Immunol. 141, 779-784, 1988
A;Title: Allogeneic manipulation of the GAT idiotypic cascade. Immunization of C57BL/6 m
A;Reference number: A92827; MUID:88285674; PMID:3135311
A;Accession: E28833
A;Molecule type: mRNA
A;Residues: 1-99 <COR>
A;Cross-references: UNIPROT:Q8VC16
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

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OM protein - protein search, using sw model

Run on: November 4, 2004, 06:45:39 ; Search time 190 Seconds
(without alignments)
21.198 Million cell updates/sec

Title: US-09-712-819D-6
Perfect score: 33
Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	86	2 Q7Z3Y5	Q7z3y5 homo sapien
2	33	100.0	102	2 AAR11040	Aar11040 mus muscu
3	33	100.0	104	2 Q9JL82	Q9jl82 mus muscu
4	33	100.0	104	2 AAR11024	Aar11024 mus muscu
5	33	100.0	104	2 AAR11056	Aar11056 mus muscu
6	33	100.0	104	2 AAR11063	Aar11063 mus muscu
7	33	100.0	105	2 AAR11074	Aar11074 mus muscu
8	33	100.0	109	2 AAR10990	Aar10990 mus muscu
9	33	100.0	112	1 KV2C_HUMAN	P01616 homo sapien
10	33	100.0	113	1 KV2D_HUMAN	P01617 homo sapien
11	33	100.0	113	1 KV2G_MOUSE	P01631 mus muscu
12	33	100.0	114	2 Q9UL80	Q9ul80 homo sapien
13	33	100.0	114	2 AAR11017	Aar11017 mus muscu
14	33	100.0	115	1 KV2A_HUMAN	P01614 homo sapien
15	33	100.0	117	1 KV2E_HUMAN	P06309 homo sapien
16	33	100.0	133	1 KV2F_HUMAN	P06310 homo sapien
17	33	100.0	148	2 Q8K122	Q8k122 mus muscu
18	33	100.0	238	2 Q99M37	Q99m37 mus muscu
19	33	100.0	238	2 Q8VCI6	Q8vci6 mus muscu
20	33	100.0	239	2 Q6P491	Q6p491 homo sapien
21	33	100.0	239	2 Q8K0F8	Q8k0f8 mus muscu
22	33	100.0	239	2 Q8VC55	Q8vc55 mus muscu
23	33	100.0	239	2 AAH63599	Aah63599 homo sapi
24	33	100.0	240	2 Q6PIH6	Q6pih6 homo sapien
25	33	100.0	240	2 AAH34142	Aah34142 homo sapi
26	31	93.9	1430	1 U13C_MOUSE	Q8k0t7 mus muscu
27	30	90.9	99	2 AAR11054	Aar11054 mus muscu
28	30	90.9	104	2 AAR11064	Aar11064 mus muscu
29	30	90.9	112	1 KV2D_MOUSE	P01629 mus muscu
30	30	90.9	112	2 Q6LEM8	Q6lem8 mus muscu
31	30	90.9	112	2 BAD00151	Bad00151 mus muscu

32	30	90.9	113	1 KV2B_HUMAN	P01615 homo sapien
33	30	90.9	113	1 KV2E_MOUSE	P03976 mus muscu
34	30	90.9	113	1 KV2F_MOUSE	P01630 mus muscu
35	30	90.9	135	2 BAC03982	Bac03982 homo sapi
36	30	90.9	239	2 Q8NEK0	Q8nek0 homo sapien
37	30	90.9	239	2 Q8TCD0	Q8tcd0 homo sapien
38	30	90.9	367	2 Q7MZU1	Q7mzu1 photorhabdu
39	30	90.9	531	1 ANM3_HUMAN	O60678 homo sapien
40	30	90.9	548	2 Q8WUV3	Q8wuv3 homo sapien
41	30	90.9	588	2 Q7QAX1	Q7qax1 anopheles g
42	30	90.9	638	2 Q46453	Q46453 clostridium
43	30	90.9	764	2 Q8IKT5	Q8ikt5 plasmodium
44	30	90.9	772	1 CIPB_CLOTM	Q01866 clostridium
45	30	90.9	1853	1 CIPA_CLOTM	Q06851 clostridium

ALIGNMENTS

RESULT 1

Q7Z3Y5
ID Q7Z3Y5 PRELIMINARY; PRT; 86 AA.
AC Q7Z3Y5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Rearranged VKA17 V gene segment (Fragment).
GN Name=VKA17;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hodgkin lymphoma;
RA Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
Hansmann M.L., Brauning A.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ564426; CAD92033.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 86
SQ SEQUENCE 86 AA; 9764 MW; D198FC04FE0C78FD CRC64;

Query Match 100.0%; Score 33; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 55 FTLKISR 61

RESULT 2

AAR11040
ID AAR11040 PRELIMINARY; PRT; 102 AA.
AC AAR11040;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.S1el; TISSUE=Spleen;
Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;

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RT "Antinuclear autoantibodies from B6.Sle1 mice.";  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY436880; AAR11040.1; -.  
FT NON_TER 1  
FT NON_TER 102  
SQ SEQUENCE 102 AA; 11112 MW; A08600D2B09ABA92 CRC64;  
  
Query Match 100.0%; Score 33; DB 2; Length 102;  
Best Local Similarity 100.0%; Pred. No. 5.4; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0;  
  
QY 1 FTLKISR 7  
Db 74 FTLKISR 80  
  
RESULT 3  
Q9JL82  
ID Q9JL82 PRELIMINARY; PRT; 104 AA.  
AC Q9JL82;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Anti-myosin immunoglobulin light chain variable region (Fragment).  
DE Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RX MEDLINE=20448942; PubMed=10992488;  
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
RT "T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin.";  
RL Infect. Immun. 68:5803-5808(2000).  
DR EMBL; AF206024; AAF69322.1; -.  
DR PIR; PLO258; PL0258.  
DR PIR; S26334; S26334.  
DR PDB; 1DLF; X-ray; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG_LIKE; 1.  
FT NON_TER 1  
FT NON_TER 104  
SQ SEQUENCE 104 AA; 11360 MW; 5DA8BBFD5FOAA1AE CRC64;  
  
Query Match 100.0%; Score 33; DB 2; Length 104;  
Best Local Similarity 100.0%; Pred. No. 5.5; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0;  
  
QY 1 FTLKISR 7  
Db 68 FTLKISR 74  
  
RESULT 4  
AAR11024  
ID AAR11024 PRELIMINARY; PRT; 104 AA.  
AC AAR11024;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE ANA immunoglobulin kappa light chain (Fragment).  
DE Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B6.Sle1; TISSUE=Spleen;  
RLiang Z., Xie C., Chen C., Kreska D., Zhou J.X., Mohan C.;  
RT "Antinuclear autoantibodies from B6.Sle1 mice.";  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY436864; AAR11024.1; -.  
FT NON_TER 1  
FT NON_TER 104  
SQ SEQUENCE 104 AA; 11310 MW; 2CF631F3058E2BB9 CRC64;  
  
Query Match 100.0%; Score 33; DB 2; Length 104;  
Best Local Similarity 100.0%; Pred. No. 5.5; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0;  
  
QY 1 FTLKISR 7  
Db 73 FTLKISR 79  
  
RESULT 5  
AAR11056  
ID AAR11056 PRELIMINARY; PRT; 104 AA.  
AC AAR11056;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE ANA immunoglobulin kappa light chain (Fragment).  
DE Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B6.Sle1; TISSUE=Spleen;  
RLiang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;  
RT "Antinuclear autoantibodies from B6.Sle1 mice.";  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY436896; AAR11056.1; -.  
FT NON_TER 1  
FT NON_TER 104  
SQ SEQUENCE 104 AA; 11327 MW; BFC116BEF36AB51A CRC64;  
  
Query Match 100.0%; Score 33; DB 2; Length 104;  
Best Local Similarity 100.0%; Pred. No. 5.5; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0;  
  
QY 1 FTLKISR 7  
Db 73 FTLKISR 79  
  
RESULT 6  
AAR11063  
ID AAR11063 PRELIMINARY; PRT; 104 AA.  
AC AAR11063;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE ANA immunoglobulin kappa light chain (Fragment).  
DE Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B6.Sle1; TISSUE=Spleen;  
RLiang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;  
RT "Antinuclear autoantibodies from B6.Sle1 mice.";  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY436903; AAR11063.1; -.  
FT NON_TER 1  
FT NON_TER 104  
SQ SEQUENCE 104 AA; 11304 MW; 9358D08600C6E65A CRC64;
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Query Match 100.0%; Score 33; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||
DB 74 FTLKISR 80

RESULT 7
AAR11074
ID AAR11074 PRELIMINARY; PRT; 105 AA.
AC AAR11074;
DT 02-MAR-2004 (TREMELrel. 27, Created)
DT 02-MAR-2004 (TREMELrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMELrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.S1el; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.S1el mice."
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436914; AAR11074.1; -.
FT NON_TER 1
FT NON_TER 105
SQ SEQUENCE 105 AA; 11378 MW; BCB358D08600CEC0 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||
DB 74 FTLKISR 80

RESULT 8
AAR10990
ID AAR10990 PRELIMINARY; PRT; 109 AA.
AC AAR10990;
DT 02-MAR-2004 (TREMELrel. 27, Created)
DT 02-MAR-2004 (TREMELrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMELrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.S1el; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.S1el mice."
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436830; AAR10990.1; -.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11894 MW; BFA0941FA01908FD CRC64;

Query Match 100.0%; Score 33; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||
DB 68 FTLKISR 74

RESULT 9
KV2C_HUMAN
ID KV2C_HUMAN STANDARD; PRT; 112 AA.
AC P01616;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region MIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Dreyer W.J., Gray W.R., Hood L.E.;
RT "The genetic, molecular, and cellular basis of antibody formation:
RT some facts and a unifying hypothesis."
RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01887; K2HUML.
DR HSPP; Q99M37; I191.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

Query Match 100.0%; Score 33; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||
DB 75 FTLKISR 81

RESULT 10
KV2D_HUMAN
ID KV2D_HUMAN STANDARD; PRT; 113 AA.
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (BENCE-JONES PROTEIN TEW).
RX MEDLINE=74148480; PubMed=4596149;
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
RT "Amino acid sequence of a kappa Bence Jones protein from a case of
RT primary amyloidosis."
RL Biochemistry 12:3763-3780(1973).
RN [2]

Query Match 100.0%; Score 33; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||
DB 75 FTLKISR 81

RA Glenner G.G.;
RT "Structural identity of Bence Jones and amyloid fibril proteins in a
RT patient with plasma cell dyscrasia and amyloidosis.";
RL J. Clin. Invest. 52:1276-1281(1973).
CC -!- MISCELLANEOUS: The major amyloid protein appears to be identical
CC with the Bence Jones protein isolated from the same patient.
CC -!- MISCELLANEOUS: This protein was isolated from the urine of a
CC patient with plasma cell dyscrasia and amyloidosis.
CC -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC marker.

DR PIR; A90370; K2HUTW.
DR HSSP; Q99M37; 1191.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Amyloid; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.

FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Framework-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81P1843CA CRC64;

Query Match 100.0%; Score 33; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 76 FTLKISR 82

RESULT 11
KV2G MOUSE STANDARD; PRT; 113 AA.
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
RT anti-digoxin hybridoma antibody.";
RL Biochemistry 22:1153-1158(1983).
CC -!- MISCELLANEOUS: This chain was isolated from an IgG2a hybridoma
CC protein that binds digoxin.
DR PIR; A01914; KVM26.
DR HSSP; Q99M37; 1191.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin V region;
KW Monoclonal antibody.

FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Framework-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match 100.0%; Score 33; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 76 FTLKISR 82

RESULT 12
Q9UL80 PRELIMINARY; PRT; 114 AA.
AC Q9UL80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035034; AAD56270.1; -.
DR PIR; B49002; B49002.
DR PIR; S23638; S23638.
DR PIR; S34094; S34094.
DR PIR; S34095; S34095.
DR HSSP; Q99M37; 1191.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 114 114
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 76 FTLKISR 82

RESULT 13
AAR11017 PRELIMINARY; PRT; 114 AA.
ID AAR11017
AC AAR11017;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).


```
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.Sle1; TISSUE=Spleen;
RA Liang Z.; Xie C.; Chen C.; Kreska D.; Hsu K.; Zhou J.X.; Mohan C.;
RT "Antinuclear autoantibodies from B6.Sle1 mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436857; AAR11017.1; --
FT NON_TER 1
FT NON_TER 114
FT NON_TER 114
SQ SEQUENCE 114 AA; 12422 MW; C94A4DDCF55E8A8C CRC64;

Query Match      100.0%; Score 33; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
   |||||
Db 73 FTLKISR 79

RESULT 14
KV2A_HUMAN
ID KV2A_HUMAN STANDARD; PRT; 115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region Cum.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RT type).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [2]
RP REVISIONS TO 50; 52; 96 AND 97.
RX MEDLINE=70063440; PubMed=4188189;
RA Hilschmann N.;
RT "Molecular basis of antibody formation.";
RL Naturwissenschaften 56:195-205(1969).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; B91639; K2HUCM.
DR HSSP; P01751; 1NQB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT NON_TER 24
FT NON_TER 115
FT NON_TER 115
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match      100.0%; Score 33; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
   |||||
```

```
Db 78 FTLKISR 84

RESULT 15
KV2E_HUMAN
ID KV2E_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobeck H.G.; Solomon A.; Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
RT diversity.";
RL Nature 309:73-76(1984).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z00009; --; NOT_ANNOTATED_CDS.
DR PIR; A01889; K2HUGM.
DR HSSP; Q99M37; 1I9I.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1
FT NON_TER 4
FT SIGNAL <1
FT CHAIN 5 117
FT DOMAIN 5 27
FT DOMAIN 28 43
FT DOMAIN 44 58
FT DOMAIN 59 65
FT DOMAIN 66 97
FT DOMAIN 98 106
FT DOMAIN 107 116
FT DISULFID 27 97
FT NON_TER 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Query Match      100.0%; Score 33; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
   |||||
Db 80 FTLKISR 86

Search completed: November 4, 2004, 06:51:41
Job time : 193 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 06:45:39 ; Search time 156 Seconds
(without alignments)
16.097 Million cell updates/sec

Title: US-09-712-819D-6
Perfect score: 33
Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	33	100.0	32	2	Aaw79207 Framework
2	33	100.0	32	4	Aab86295 Murine de
3	33	100.0	32	5	Abp62672 Human imm
4	33	100.0	32	5	Abp62674 Human imm
5	33	100.0	32	5	Aau70400 Human lig
6	33	100.0	32	5	Aau70440 Mouse lig
7	33	100.0	32	7	Adm08541 Canine im
8	33	100.0	32	7	Adm08539 Canine im
9	33	100.0	32	8	Adl93640 Human CD4
10	33	100.0	32	8	Adl93554 Human CD4
11	33	100.0	37	8	Adg31286 Humanised
12	33	100.0	50	5	Abg30477 Human ant
13	33	100.0	50	5	Abg30478 Human ant
14	33	100.0	50	5	Abg30479 Human ant
15	33	100.0	81	2	Aar92994 Homologou
16	33	100.0	89	2	Aar80082 Mouse der
17	33	100.0	91	6	Abf55905 Human mAb
18	33	100.0	91	6	Abf55889 Human mAb
19	33	100.0	92	2	Aar27009 Hypercalc
20	33	100.0	93	3	Aay56670 Partial p
21	33	100.0	96	7	Adc99843 Anti-huma
22	33	100.0	96	7	Add05447 Anti-MUC1
23	33	100.0	96	7	Adf09885 Anti-MUC1
24	33	100.0	99	7	Adk18941 Anti-huma
25	33	100.0	99	7	Adk18899 Anti-huma

26	33	100.0	99	7	ADK18857	Adk18857 Anti-huma
27	33	100.0	99	7	ADJ80416	Adj80416 Hybrid hu
28	33	100.0	100	2	AAR72067	Aar72067 OF7K.7 VK
29	33	100.0	100	2	AAR72066	Aar72066 VK005 VK
30	33	100.0	100	4	AAE12711	AAe12711 Antibody
31	33	100.0	100	4	AAE06959	AAe06959 Mouse ger
32	33	100.0	100	4	AAE06964	AAe06964 Mouse ger
33	33	100.0	100	4	AAE06960	AAe06960 Mouse ger
34	33	100.0	100	4	AAE06962	AAe06962 Mouse ger
35	33	100.0	100	4	AAE06963	AAe06963 Mouse ger
36	33	100.0	100	4	AAE06958	AAe06958 Murine 1D
37	33	100.0	100	4	AAE06967	AAe06967 Mouse ger
38	33	100.0	100	4	AAE06966	AAe06966 Mouse ger
39	33	100.0	100	4	AAE06965	AAe06965 Mouse ger
40	33	100.0	100	4	AAE06961	AAe06961 Mouse ger
41	33	100.0	100	5	ABG76927	Abg76927 Humanised
42	33	100.0	100	6	AAE35909	AAe35909 Human A3/
43	33	100.0	100	6	AAE35907	AAe35907 Human A17
44	33	100.0	100	6	ABU58803	Abu58803 Mucin 1 (
45	33	100.0	100	6	ABJ18695	Abj18695 Antibody

ALIGNMENTS

RESULT 1
AAW79207
ID AAW79207 standard; protein; 32 AA.

XX AAW79207;

AC AAW79207;

DT 21-DEC-1998 (first entry)

DE Framework 3 region of human V kappa gene HUM5400.

XX Monoclonal antibody; MAb; LO-CD2a; humanised antibody; CD2 antigen;

KW human lymphocyte; immune response; chimeric; graft-versus-host disease;

KW T-cell; transplant rejection; autoimmune disease; HUM5400.

XX Homo sapiens.

OS US5817311-A.

PN 06-OCT-1998.

PD 07-JUN-1995; 95US-00472281.

XX 05-MAR-1993; 93US-00027008.

PR 09-SEP-1993; 93US-00119032.

PR 29-MAR-1995; 95US-00407009.

XX (UYLO-) UNIV CATHOLIQUE LOUVAIN.

PI Latine D, Bazin H;

XX WPI; 1998-556337/47.

XX Inhibition of T-cell mediated immune response with anti-CD2 monoclonal

PT antibody LO-CD2a - used for preventing transplant rejection or for

PT treating graft-versus-host disease or auto-immune diseases.

XX Example 7; Col 33-34; 96pp; English.

XX This represents the amino acid sequence of the framework 3 region of

CC human V kappa gene HUM5400. This is used to construct a humanised antibody

CC LO-CD2a. The invention relates to the use of the monoclonal antibody

CC (MAb) LO-CD2a or a humanised or a chimeric version of the LO-CD2a

CC antibody for the inhibition of a T-cell mediated immune response in a

CC patient. The MAb LO-CD2a (produced by hybridoma cell line ATCC HB 11423)

CC can bind to an epitope on the CD2 antigen of the human lymphocytes. The T

CC -cell mediated immune response in a patient can be inhibited by

CC administering the MAb LO-CD2a or an antibody that binds to the same human

CC lymphocyte epitope as LO-CD2a. The method is used for preventing

DE Human immunopeptide to HCV E2 glycoprotein framework sequence #182.
XX Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW NS3 protein; viral infection.
XX Homo sapiens.
XX WO200259340-A1.
XX 01-AUG-2002.
XX 25-JAN-2002; 2002WO-US002303.
XX 26-JAN-2001; 2001US-0264451P.
XX (SCRI) SCRIPPS RES INST.
XX Maruyama T, Jones IM, Burton DR, Fox RI;
XX WPI; 2002-599801/64.
XX New human immunopolypeptide with binding specificity for certain envelope
PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
PT diagnosing or treating patients having or suspected of having HCV
PT infection.
XX Claim 4; Fig 17; 308pp; English.
PS The present invention relates to human immunopolypeptides, produced by a
XX phage transfected cell library. The present sequence is one such
CC immunopolypeptide. The immunopolypeptides have binding specificity for
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC virus (HCV). E2 glycoprotein is believed to be responsible for target
CC cell binding and contains neutralising epitopes, while NS3 is thought to
CC be involved in the replication of HCV. The immunopolypeptides are useful
CC for diagnosing and treating a patient having or suspected to be having
XX HCV infection
XX SQ Sequence 32 AA;
Query Match 100.0%; Score 33; DB 5; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
Db 15 FTLKISR 21
RESULT 5
AAU70400
ID AAU70400 standard; peptide; 32 AA.
XX AAU70400;
XX 14-FEB-2002 (first entry)
XX Human light chain immunoglobulin framework region 3 #2.
XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
KW complementarity determining region; framework region; IgBP;
KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
KW IgD; IgE; IgM; kappa; lambda; CHBP.
XX Homo sapiens.
OS WO200183806-A1.
XX 08-NOV-2001.
XX 02-MAY-2001; 2001WO-US014349.
XX

DE Human immunopeptide to HCV E2 glycoprotein framework sequence #182.
XX Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW NS3 protein; viral infection.
XX Homo sapiens.
XX WO200259340-A1.
XX 01-AUG-2002.
XX 25-JAN-2002; 2002WO-US002303.
XX 26-JAN-2001; 2001US-0264451P.
XX (SCRI) SCRIPPS RES INST.
XX Maruyama T, Jones IM, Burton DR, Fox RI;
XX WPI; 2002-599801/64.
XX New human immunopolypeptide with binding specificity for certain envelope
PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
PT diagnosing or treating patients having or suspected of having HCV
PT infection.
XX Claim 4; Fig 17; 308pp; English.
PS The present invention relates to human immunopolypeptides, produced by a
XX phage transfected cell library. The present sequence is one such
CC immunopolypeptide. The immunopolypeptides have binding specificity for
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC virus (HCV). E2 glycoprotein is believed to be responsible for target
CC cell binding and contains neutralising epitopes, while NS3 is thought to
CC be involved in the replication of HCV. The immunopolypeptides are useful
CC for diagnosing and treating a patient having or suspected to be having
XX HCV infection
XX SQ Sequence 32 AA;
Query Match 100.0%; Score 33; DB 5; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
Db 15 FTLKISR 21
RESULT 6
AAU70440
ID AAU70440 standard; peptide; 32 AA.
XX AAU70440;
XX 14-FEB-2002 (first entry)
XX Mouse light chain immunoglobulin framework region 3 #2.
XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
KW complementarity determining region; framework region; IgBP;
KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
KW IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
XX Mus musculus.
OS WO200183806-A1.
XX 08-NOV-2001.
XX 02-MAY-2001; 2001WO-US014349.
XX 02-MAY-2000; 2000US-00563222.
XX (EPIC-) EPICYTE PHARM INC.
XX Hiatt AC, Hein MB;
XX WPI; 2002-055482/07.

PR 02-MAY-2000; 2000US-00563222.
XX (EPIC-) EPICYTE PHARM INC.
PA Hiatt AC, Hein MB;
PI WPI; 2002-055482/07.
XX Preparing immunoglobulin binding protein array in plant cells by
XX transforming the cells with different polynucleotides encoding binding
XX protein polypeptides specific to ligand, selecting plant cells for
XX preparing array.
PS Disclosure; Fig 1A; 129pp; English.
XX The invention relates to transforming a population of cells (e.g. plant
CC cells), comprising using a library of two different polynucleotides
CC encoding different immunoglobulin binding protein (IgBP) polypeptides
CC that specifically bind to a ligand or form one or more disulphide bonds
CC with polypeptides in transfected cells, to generate an IgBP that binds to
CC a ligand, and transformed plant cells are selected, and preparing an IgBP
CC array in plant cells. At least one peptide sequence has at least 75%
CC sequence identity to a framework region (FR) of a native IGM, IGG, IGA,
CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
CC useful for preparing an immunoglobulin binding protein array, preferably
CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
CC discovery of e.g. screening assays of IGBPs having desired
CC characteristics. The present sequence is a mammalian immunoglobulin
CC derived peptide that may be incorporated into an IgBP of the invention
XX SQ Sequence 32 AA;
Query Match 100.0%; Score 33; DB 5; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
Db 15 FTLKISR 21
RESULT 6
AAU70440
ID AAU70440 standard; peptide; 32 AA.
XX AAU70440;
XX 14-FEB-2002 (first entry)
XX Mouse light chain immunoglobulin framework region 3 #2.
XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
KW complementarity determining region; framework region; IgBP;
KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
KW IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
XX Mus musculus.
OS WO200183806-A1.
XX 08-NOV-2001.
XX 02-MAY-2001; 2001WO-US014349.
XX 02-MAY-2000; 2000US-00563222.
XX (EPIC-) EPICYTE PHARM INC.
XX Hiatt AC, Hein MB;
XX WPI; 2002-055482/07.

XX Preparing immunoglobulin binding protein array in plant cells by
PT transforming the cells with different polynucleotides encoding binding
PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array.
XX
PS Disclosure; Fig 1A; 129pp; English.
XX
CC The invention relates to transforming a population of cells (e.g. plant
CC cells), comprising using a library of two different polynucleotides
CC encoding different immunoglobulin binding protein (IgBP) polypeptides
CC that specifically bind to a ligand or form one or more disulphide bonds
CC with polypeptides in transfected cells, to generate an IgBP that binds to
CC a ligand, and transformed plant cells are selected, and preparing an IgBP
CC array in plant cells. At least one peptide sequence has at least 75%
CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
CC useful for preparing an immunoglobulin binding protein array, preferably
CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
CC discovery of e.g. screening assays of IgBPs having desired
CC characteristics. The present sequence is a mammalian immunoglobulin
CC derived peptide that may be incorporated into an IgBP of the invention
XX
SQ Sequence 32 AA;
Query Match 100.0%; Score 33; DB 5; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
Db 15 FTLKISR 21
RESULT 7
ADM08541
ID ADM08541 standard; peptide; 32 AA.
XX
AC ADM08541;
XX
DT 20-MAY-2004 (first entry)
XX
DE Canine immunoglobulin kappa VL subgenus framework 3 peptide 18.
XX
KW canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
KW antiallergic; allergy; IgE; gene therapy; kappa subgenus; VL framework;
KW FR3.
XX
OS Canis familiaris.
XX
PN WO2003060080-A2.
XX
PD 24-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-US041362.
XX
PR 21-DEC-2001; 2001US-0344874P.
XX
PA (IDEX-) IDEXX LAB INC.
XX
PI Krah ER, Guo H, Aiyappa A, Lawton R;
XX
DR WPI; 2003-598521/56.
XX
CC The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates
CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (FR) peptide of the
CC invention.
XX
PS Claim 42; Page 109; 130pp; English.
XX
CC The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates
XX
PS Claim 42; Page 109; 130pp; English.
XX
CC The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates

CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (FR) peptide of the
CC invention.
XX
SQ Sequence 32 AA;
Query Match 100.0%; Score 33; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
Db 15 FTLKISR 21
RESULT 8
ADM08539
ID ADM08539 standard; peptide; 32 AA.
XX
AC ADM08539;
XX
DT 20-MAY-2004 (first entry)
XX
DE Canine immunoglobulin kappa VL subgenus framework 3 peptide 16.
XX
KW canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
KW antiallergic; allergy; IgE; gene therapy; kappa subgenus; VL framework;
KW FR3.
XX
OS Canis familiaris.
XX
PN WO2003060080-A2.
XX
PD 24-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-US041362.
XX
PR 21-DEC-2001; 2001US-0344874P.
XX
PA (IDEX-) IDEXX LAB INC.
XX
PI Krah ER, Guo H, Aiyappa A, Lawton R;
XX
DR WPI; 2003-598521/56.
XX
CC New canine heavy and light chain variable domain polypeptides, useful for
CC treating canine allergy.
XX
PS Claim 42; Page 109; 130pp; English.
XX
CC The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates
CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (FR) peptide of the
CC invention.
XX
SQ Sequence 32 AA;
Query Match 100.0%; Score 33; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
Db 15 FTLKISR 21
RESULT 9
ADL93640
ID ADL93640 standard; peptide; 32 AA.
XX

```
AC ADL93640;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human CD44-binding antibody FR3-L SEQ ID NO:135.
XX
KW human; CD44; light chain immunoglobulin variable domain;
KW heavy chain immunoglobulin variable domain; immunoglobulin; cytotstatic;
KW antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;
KW dermatological; vasotropic; neuroprotective; antibody therapy;
KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;
KW graft versus host response; multiple sclerosis; neoplastic disorder;
KW cancer; antibody.
XX
OS Homo sapiens.
XX
PN WO2004024750-A2.
XX
PD 25-MAR-2004.
XX
XX 15-SEP-2003; 2003WO-US029318.
XX
PF 13-SEP-2002; 2002US-0410758P.
XX
PR 09-MAY-2003; 2003US-0469123P.
XX
XX (DYAX-) DYAX CORP.
XX
PA Rondon IJ, Edge A, Baribault Kent R;
XX
PI WPI; 2004-270003/25.
XX
DR New protein comprising a light chain (LC) immunoglobulin variable domain
XX sequence and a heavy chain (HC) immunoglobulin variable domain sequence,
XX useful for preparing a composition for treating inflammatory or
XX neoplastic disorders.
XX
PS Disclosure; SEQ ID NO 135; 128pp; English.
XX
CC The invention relates to a novel isolated protein comprising a light
CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)
CC immunoglobulin variable domain sequence that form an antigen binding site
CC with binding affinity for the human CD44 extracellular domain and where
CC CDR3 of the LC variable domain sequence. A protein of the invention has
CC cytotstatic, antiinflammatory, immunosuppressive, antiarthritic,
CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,
CC and may have a use in antibody therapy. The protein is useful for
CC preparing a composition for treating inflammatory disorders, e.g.,
CC rheumatoid arthritis, lupus, restenosis, graft versus host response or
CC multiple sclerosis or neoplastic disorder, which is a malignant or
CC metastatic cancer. The present sequence represents a framework (FR)
CC domain of a human CD44-binding antibody of the invention.
XX
SQ Sequence 32 AA;

Query Match 100.0%; Score 33; DB 8; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 10
ADL93554
ID ADL93554 standard; peptide; 32 AA.
XX
AC ADL93554;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human CD44-binding antibody H10 VLC FR3 SEQ ID NO:49.
XX

human; CD44; light chain immunoglobulin variable domain;
heavy chain immunoglobulin variable domain; immunoglobulin; cytotstatic;
antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;
dermatological; vasotropic; neuroprotective; antibody therapy;
inflammatory disorders; rheumatoid arthritis; lupus; restenosis;
graft versus host response; multiple sclerosis; neoplastic disorder;
cancer; antibody.
Homo sapiens.
WO2004024750-A2.
25-MAR-2004.
15-SEP-2003; 2003WO-US029318.
13-SEP-2002; 2002US-0410758P.
09-MAY-2003; 2003US-0469123P.
(DYAX-) DYAX CORP.
Rondon IJ, Edge A, Baribault Kent R;
WPI; 2004-270003/25.
New protein comprising a light chain (LC) immunoglobulin variable domain
sequence and a heavy chain (HC) immunoglobulin variable domain sequence,
useful for preparing a composition for treating inflammatory or
neoplastic disorders.
Disclosure; SEQ ID NO 135; 128pp; English.
The invention relates to a novel isolated protein comprising a light
chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)
immunoglobulin variable domain sequence that form an antigen binding site
with binding affinity for the human CD44 extracellular domain and where
CDR3 of the LC variable domain sequence. A protein of the invention has
cytotstatic, antiinflammatory, immunosuppressive, antiarthritic,
antirheumatic, dermatological, vasotropic, and neuroprotective activity,
and may have a use in antibody therapy. The protein is useful for
preparing a composition for treating inflammatory disorders, e.g.,
rheumatoid arthritis, lupus, restenosis, graft versus host response or
multiple sclerosis or neoplastic disorder, which is a malignant or
metastatic cancer. The present sequence represents a framework (FR)
domain of a human CD44-binding antibody of the invention.
Sequence 32 AA;

Query Match 100.0%; Score 33; DB 8; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 11
ADQ31286
ID ADQ31286 standard; peptide; 37 AA.
XX
AC ADQ31286;
XX
DT 09-SEP-2004 (first entry)
XX
DE Humanised murine 1A1 light chain antibody peptide SeqID 52.
XX
KW 1A1; monocyte chemotactic protein; beta-chemokine family;
KW glomerulonephritis; scleroderma; cirrhosis; multiple sclerosis;
KW lupus nephritis; atherosclerosis; inflammatory bowel disease;
KW rheumatoid arthritis; inflammatory disease; fibrotic disorder; cancer;
KW immunopathological disorder; antiarteriosclerotic; antiarthritic;
KW antiinflammatory; antirheumatic; cytotstatic; dermatological;
```


XXKWhepatotropic; immunomodulator; nephrotropic; neuroprotective; mouse; MCP; murine; humanised antibody.

XXOSMus musculus.

XXOSSynthetic.

XXPNWO2004050836-A2.

XXPD17-JUN-2004.

XXPF25-NOV-2003; 2003WO-US037834.

XXPR27-NOV-2002; 2002US-0430007P.

XXPA(BIOG-) BIOGEN IDEC MA INC.

XXPIDe Fougerolles AR, Kotelianski VE, Garber E, Reid C, Saldanha JW, Van Vlijmen H;

XXXWPWI; 2004-461110/43.

XXPTNew antibodies against monocyte chemotactic proteins (MCP), useful for treating or preventing disorders associated with detrimental MCP activity, e.g. glomerulonephritis, scleroderma, multiple sclerosis, or atherosclerosis.

XXPSDisclosure; SEQ ID NO 52; 200pp; English.

XXCCThis invention relates to an antibody for treating or preventing disorders associated with detrimental monocyte chemotactic protein (MCP) activity. Specifically, it refers to humanised antibodies that bind to members of the beta-chemokine family (of which MCP-1, MCP-2 and MCP-3 belong) and in particular antibodies that have been modelled on, and modified from, the variable complementarity determining regions (CDRs) of the murine 11K2 and 1A1 immunoglobulin sequences. The present invention describes using these antibodies to treat or prevent diseases and disorders including glomerulonephritis, scleroderma, cirrhosis, multiple sclerosis, lupus nephritis, atherosclerosis, inflammatory bowel diseases, rheumatoid arthritis, inflammatory diseases, fibrotic disorders, cancer and immunopathological disorders. Accordingly, they can be used in the development of pharmaceutical compositions that exhibit antiarteriosclerotic, antiarthritic, antiinflammatory, antirheumatic, cytostatic, dermatological, hepatotropic, immunomodulator, nephrotropic and neuroprotective activities. This peptide sequence is the humanised murine 1A1 variable and constant light chain antibody peptide of the invention.

XXSQSequence 37 AA;

Query Match100.0%; Score 33; DB 8; Length 37;

Best Local Similarity100.0%; Pred. No. 4.3;

Matches7; Conservative0; Mismatches0; Indels0; Gaps0;

QY1 FTLKISR 7

DB1 FTLKISR 7

RESULT 12

ABG30477

IDABG30477 standard; protein; 50 AA.

XXACABG30477;

XXDT07-OCT-2002 (first entry)

XXDEHuman anti-CD40 monoclonal antibody 5H7 light chain #2.

XXKWHuman; light chain; CD40; autoimmune disease; multiple sclerosis;

XXKWsystemic lupus erythematosus; psoriasis; inflammatory bowel disease;

XXKWCrohn's disease; rheumatoid arthritis; organ rejection; lymphoma;

XXKWnon-Hodgkin's lymphoma; monoclonal antibody; B cell; glycoprotein; proliferation.

XXOSHomo sapiens.

XXPNWO200228904-A2.

XXPD11-APR-2002.

XXPF02-OCT-2001; 2001WO-US030857.

XXPR02-OCT-2000; 2000US-0237556P.

XXPA(CHIR) CHIRON CORP.

XXPIChu K, Wang C, Yoshihara C, Donnelly JJ;

XXXWPWI; 2002-405169/43.

XXPTA human anti-CD40 monoclonal antibody or fragment useful for inhibiting proliferation, growth or differentiation of a normal human B cells and treating autoimmune disease such as rheumatoid arthritis or systemic lupus erythematosus.

XXPSClaim 1; Fig 5; 75pp; English.

XXCCThe invention relates to a human monoclonal antibody or fragment capable of specifically binding to a human CD40 antigen (a glycoprotein expressed on the surface of human B cells), where the antibody or fragment is free of significant agonistic activity when it binds to the CD40 antigen, and the growth or differentiation is inhibited. The fragments comprise the complementarity determining region (CDR) of the light and heavy chains of the monoclonal antibodies secreted by a hybridoma consisting of 15B8, 20C4, 12D9, 9P7 and 13E4. Also included are the nucleic acids encoding the antibody (or fragments). The antibodies or fragments are used for inhibiting proliferation, growth or differentiation of a normal human B cells and to inhibit antibody production by B cells. They may also be useful for treating autoimmune diseases, such as systemic lupus erythematosus, psoriasis, multiple sclerosis, inflammatory bowel disease (Crohn's disease), rheumatoid arthritis, and lymphoma (especially Non-Hodgkin's lymphoma). The present sequence represents the antibody 5H7 (another anti-CD40 antibody) light chain

XXSQSequence 50 AA;

Query Match100.0%; Score 33; DB 5; Length 50;

Best Local Similarity100.0%; Pred. No. 5.8;

Matches7; Conservative0; Mismatches0; Indels0; Gaps0;

QY1 FTLKISR 7

DB15 FTLKISR 21

RESULT 13

ABG30478

IDABG30478 standard; protein; 50 AA.

XXACABG30478;

XXDT07-OCT-2002 (first entry)

XXDEHuman anti-CD40 monoclonal antibody 9F7 light chain #2.

XXKWHuman; light chain; CD40; autoimmune disease; multiple sclerosis;

XXKWsystemic lupus erythematosus; psoriasis; inflammatory bowel disease;

XXKWCrohn's disease; rheumatoid arthritis; organ rejection; lymphoma;

XXKWnon-Hodgkin's lymphoma; monoclonal antibody; B cell; glycoprotein; proliferation.

XXOSHomo sapiens.

XXXW200228904-A2.

XXPD11-APR-2002.

XX 02-OCT-2001; 2001WO-US030857.
XX
PR 02-OCT-2000; 2000US-0237556P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Chu K, Wang C, Yoshihara C, Donnelly JJ;
XX WPI; 2002-405169/43.
XX
PT A human anti-CD40 monoclonal antibody or fragment useful for inhibiting
PT proliferation, growth or differentiation of a normal human B cells and
PT treating autoimmune disease such as rheumatoid arthritis or systemic
XX lupus erythematosus.
PS Claim 1; Fig 5; 75pp; English.
XX
CC The invention relates to a human monoclonal antibody or fragment capable
CC of specifically binding to a human CD40 antigen (a glycoprotein expressed
CC on the surface of human B cells), where the antibody or fragment is free
CC of significant agonistic activity when it binds to the CD40 antigen, and
CC the growth or differentiation is inhibited. The fragments comprise the
CC complementarity determining region (CDR) of the light and heavy chains of
CC the monoclonal antibodies secreted by a hybridoma consisting of 15B8,
CC 20C4, 12D9, 9F7 and 13E4. Also included are the nucleic acids encoding
CC the antibody (or fragments). The antibodies or fragments are used for
CC inhibiting proliferation, growth or differentiation of a normal human B
CC cells and to inhibit antibody production by B cells. They may also be
CC useful for treating autoimmune diseases, such as systemic lupus
CC erythematosus, psoriasis, multiple sclerosis, inflammatory bowel disease
CC (Crohn's disease), rheumatoid arthritis, and lymphoma (especially Non-
CC Hodgkin's lymphoma). The present sequence represents the antibody 9F7
CC light chain
XX
SQ Sequence 50 AA;

Query Match 100.0%; Score 33; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db |||||
15 FTLKISR 21

RESULT 14
ABG30479
ID ABG30479 standard; protein; 50 AA.
XX
AC ABG30479;
XX
DT 07-OCT-2002 (first entry)
DE
XX Human anti-CD40 monoclonal antibody 15B8 light chain #2.
KW Human; light chain; CD40; autoimmune disease; multiple sclerosis;
KW systemic lupus erythematosus; psoriasis; inflammatory bowel disease;
KW Crohn's disease; rheumatoid arthritis; organ rejection; lymphoma;
KW non-Hodgkin's lymphoma; monoclonal antibody; B cell; glycoprotein;
KW proliferation.
XX
OS Homo sapiens.
XX
FN WO200228904-A2.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US030857.
XX
PR 02-OCT-2000; 2000US-0237556P.
XX
PA (CHIR) CHIRON CORP.

XX Chu K, Wang C, Yoshihara C, Donnelly JJ;
PI WPI; 2002-405169/43.
XX
PT A human anti-CD40 monoclonal antibody or fragment useful for inhibiting
PT proliferation, growth or differentiation of a normal human B cells and
PT treating autoimmune disease such as rheumatoid arthritis or systemic
PT lupus erythematosus.
XX
PS Claim 1; Fig 5; 75pp; English.
XX
CC The invention relates to a human monoclonal antibody or fragment capable
CC of specifically binding to a human CD40 antigen (a glycoprotein expressed
CC on the surface of human B cells), where the antibody or fragment is free
CC of significant agonistic activity when it binds to the CD40 antigen, and
CC the growth or differentiation is inhibited. The fragments comprise the
CC complementarity determining region (CDR) of the light and heavy chains of
CC the monoclonal antibodies secreted by a hybridoma consisting of 15B8,
CC 20C4, 12D9, 9F7 and 13E4. Also included are the nucleic acids encoding
CC the antibody (or fragments). The antibodies or fragments are used for
CC inhibiting proliferation, growth or differentiation of a normal human B
CC cells and to inhibit antibody production by B cells. They may also be
CC useful for treating autoimmune diseases, such as systemic lupus
CC erythematosus, psoriasis, multiple sclerosis, inflammatory bowel disease
CC (Crohn's disease), rheumatoid arthritis, and lymphoma (especially Non-
CC Hodgkin's lymphoma). The present sequence represents the antibody 15B8
CC light chain
XX
SQ Sequence 50 AA;

Query Match 100.0%; Score 33; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db |||||
15 FTLKISR 21

RESULT 15
AAR92994
ID AAR92994 standard; protein; 81 AA.
XX
AC AAR92994;
XX
DT 25-MAR-2003 (revised)
DT 18-MAY-1996 (first entry)
XX
DE Homologous sequences to antibody IOR-R3 variable region light chain.
XX
KW IOR-R3; monoclonal antibody; human; mouse; light chain; homology;
KW variable region; epidermal growth factor receptor; hybridoma; framework;
KW cloning; computer; algorithm; immunogenicity; site-directed mutagenesis;
KW T-lymphocyte epitope; tertiary structure; point mutation;
KW antibody engineering; protein engineering; humanised antibody;
KW antitumour; cancer; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 2 /note= "Amino acid involved in tertiary structure"
FT Region 4 /note= "Amino acid involved in tertiary structure"
FT Region 24. .25 /note= "Amino acids involved in tertiary structure"
FT Region 35. .39 /note= "Amino acids involved in tertiary structure"
FT Region 46 /note= "Amino acid involved in tertiary structure"
FT Region 48 /note= "Amino acid involved in tertiary structure"
FT Region /note= "Amino acid involved in tertiary structure"

FT Region 50. 51
FT /note= "Amino acids involved in tertiary structure"
FT 53
FT Region /note= "Amino acid involved in tertiary structure"
FT 71
FT Region /note= "Amino acid involved in tertiary structure"
XX
PN EP699755-A2.
XX
PD 06-MAR-1996.
XX
PF 27-JUN-1995; 95EP-00201752.
XX
PR 30-JUN-1994; 94CU-00000080.
XX
PA (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
XX
PI Rodriguez RP, Valladares JL, Mateo De Acosta Del Rio CM;
XX
DR WPI; 1996-130770/14.
XX
PT Identifying interspecies differences in amino acid sequence of Ig T-cell
PT epitopes - by sequence comparison, also humanised antibodies contg.
PT altered T-cell epitopes, retaining antigen specificity but not
PT immunogenicity, esp. for tumour treatment.
XX
PS Claim 14; Fig 3; 33pp; English.
XX
CC The sequence represents residues from a human immunoglobulin with
CC homology to the light chain variable region from monoclonal antibody IOR-
CC R3 (AAR92993), specific for epidermal growth factor receptor, produced by
CC a mouse hybridoma. The sequence is partial, and complementarity
CC determining regions are omitted. The sequence is isolated by comparison
CC of human and mouse immunoglobulins and analysis for T-lymphocyte
CC antigenic sequences using a computer algorithm. Residues not within a
CC complementarity determining region, canonical structure or Vernier zone
CC may be modified to reduce immunogenicity in humans (e.g. in sequence
CC AAR92995). This method, which involves the introduction of only a few
CC point mutations into T-cell epitope coding regions, is generally
CC applicable in humanisation of mouse antibodies. The resulting humanised
CC antibodies may be used e.g. as antitumour agents. They retain the antigen
CC recognition of the original antibody, but are not immunogenic in humans.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 81 AA;

Query Match 100.0%; Score 33; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db |||||
53 FTLKISR 59

Search completed: November 4, 2004, 06:48:24
Job time : 158 secs

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OM protein - protein search, using sw model

Run on: November 4, 2004, 06:51:47 ; Search time 142 Seconds
(without alignments)
17.413 Million cell updates/sec

Title: US-09-712-819D-6
Perfect score: 33
Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 353225886 residues

Total number of hits satisfying chosen parameters: 1566620

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	33	100.0	32	10	US-09-563-222-80
2	33	100.0	32	10	US-09-563-222-120
3	33	100.0	32	10	US-09-947-839-71
4	33	100.0	32	14	US-10-168-809-5
5	33	100.0	32	16	US-10-663-244-49
6	33	100.0	32	16	US-10-663-244-135
7	33	100.0	32	16	US-10-327-598-385
8	33	100.0	32	16	US-10-327-598-389
9	33	100.0	32	17	US-10-783-950-80
10	33	100.0	32	17	US-10-783-950-114
11	33	100.0	93	9	US-09-905-243-61
12	33	100.0	99	14	US-10-041-860-281
13	33	100.0	99	14	US-10-041-860-323

14	33	100.0	99	14	US-10-041-860-365	Sequence 365, App
15	33	100.0	99	14	US-10-308-817-176	Sequence 176, App
16	33	100.0	99	15	US-10-453-698-176	Sequence 176, App
17	33	100.0	100	9	US-09-822-698A-19	Sequence 19, Appl
18	33	100.0	100	9	US-09-840-459-21	Sequence 21, Appl
19	33	100.0	100	9	US-09-840-459-22	Sequence 22, Appl
20	33	100.0	100	9	US-09-840-459-23	Sequence 23, Appl
21	33	100.0	100	9	US-09-840-459-24	Sequence 24, Appl
22	33	100.0	100	9	US-09-840-459-25	Sequence 25, Appl
23	33	100.0	100	9	US-09-840-459-26	Sequence 26, Appl
24	33	100.0	100	9	US-09-840-459-27	Sequence 27, Appl
25	33	100.0	100	9	US-09-840-459-28	Sequence 28, Appl
26	33	100.0	100	9	US-09-840-459-29	Sequence 29, Appl
27	33	100.0	100	9	US-09-840-459-30	Sequence 30, Appl
28	33	100.0	100	14	US-10-194-975-75	Sequence 75, Appl
29	33	100.0	100	14	US-10-194-975-76	Sequence 76, Appl
30	33	100.0	100	14	US-10-194-975-77	Sequence 77, Appl
31	33	100.0	100	14	US-10-194-975-78	Sequence 78, Appl
32	33	100.0	100	14	US-10-194-975-79	Sequence 79, Appl
33	33	100.0	100	14	US-10-194-975-80	Sequence 80, Appl
34	33	100.0	100	14	US-10-194-975-81	Sequence 81, Appl
35	33	100.0	100	14	US-10-125-687-24	Sequence 24, Appl
36	33	100.0	100	14	US-10-153-382-36	Sequence 36, Appl
37	33	100.0	100	14	US-10-153-382-38	Sequence 38, Appl
38	33	100.0	100	14	US-10-041-860-8	Sequence 8, Appl
39	33	100.0	100	14	US-10-041-860-280	Sequence 280, App
40	33	100.0	100	14	US-10-041-860-321	Sequence 321, App
41	33	100.0	100	14	US-10-041-860-364	Sequence 364, App
42	33	100.0	100	14	US-10-010-942B-7	Sequence 7, Appl
43	33	100.0	100	14	US-10-308-817-22	Sequence 22, Appl
44	33	100.0	100	14	US-10-308-817-23	Sequence 23, Appl
45	33	100.0	100	14	US-10-308-817-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-563-222-80
; Sequence 80, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-563-222-80

Query Match 100.0%; Score 33; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 2
US-09-563-222-120
; Sequence 120, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.

```

; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-120

Query Match      100.0%; Score 33; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLKISR 7
       |||||
Db      15 FTLKISR 21

RESULT 3
US-09-947-839-71
; Sequence 71, Application US/09947839
; Publication No. US20030138428A1
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; Ceriani Dr., Roberto L.
; Peterson Dr., Jerry A.
; Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; Carcinoma Specificity, and Kit and
; Diagnostic Vaccination and
; Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski
; STREET: 444 South Flower St., 19th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/947,839
; FILING DATE: 06-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/976,288
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 07/977,696
; FILING DATE: No. US20030138428A1ember 16, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Anzel Ph.D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P6639938
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-09-947-839-71

; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-120

Query Match      100.0%; Score 33; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLKISR 7
       |||||
Db      15 FTLKISR 21

RESULT 4
US-10-168-809-5
; Sequence 5, Application US/10168809
; Publication No. US20030180799A1
; GENERAL INFORMATION:
; APPLICANT: Muller-Hermelink, Hans Konrad
; APPLICANT: GREINER, AXEL
; APPLICANT: DORKEN, BERND
; APPLICANT: BARGOU, RALF
; APPLICANT: KUPER, PETER
; TITLE OF INVENTION: ANTIBODIES AGAINST PLASMA CELLS
; FILE REFERENCE: 009848-0272298
; CURRENT APPLICATION NUMBER: US/10/168,809
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: PCT/EP00/13238
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: DE 199 62 583.2
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic hybrid, no
; OTHER INFORMATION: natural origin
US-10-168-809-5

Query Match      100.0%; Score 33; DB 14; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLKISR 7
       |||||
Db      15 FTLKISR 21

RESULT 5
US-10-663-244-49
; Sequence 49, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-49
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Query Match 100.0%; Score 33; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||
Db 15 FTLKISR 21

RESULT 6

US-10-663-244-135
; Sequence 135, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-135

Query Match 100.0%; Score 33; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||
Db 15 FTLKISR 21

RESULT 7

US-10-327-598-385
; Sequence 385, Application US/10327598
; Publication No. US20040181039A1
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 385
; LENGTH: 32
; TYPE: PRT
; ORGANISM: canis familiaris;
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (31)..(31)
; OTHER INFORMATION: X is Y, H, F, or C
US-10-327-598-385

Query Match 100.0%; Score 33; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||
Db 15 FTLKISR 21

RESULT 8

US-10-327-598-389
; Sequence 389, Application US/10327598
; Publication No. US20040181039A1
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 389
; LENGTH: 32
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-389

Query Match 100.0%; Score 33; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||
Db 15 FTLKISR 21

RESULT 9

US-10-783-950-80
; Sequence 80, Application US/10783950
; Publication No. US20040199945A1
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, NICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/10/783,950
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US/09/563,222
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-783-950-80

Query Match 100.0%; Score 33; DB 17; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7

Db	15 FTLKISR 21	76 FTLKISR 82	
RESULT 10			
US-10-783-950-114			
; Sequence 114, Application US/10783950			
; Publication No. US20040199945A1			
; GENERAL INFORMATION:			
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.			
; APPLICANT: HIATT, ANDREW C.			
; APPLICANT: HEIN, MICH B.			
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS			
; FILE REFERENCE: 068904-0501			
; CURRENT APPLICATION NUMBER: US/10/783,950			
; CURRENT FILING DATE: 2004-02-19			
; PRIOR APPLICATION NUMBER: US/09/563,222			
; PRIOR FILING DATE: 2000-05-02			
; PRIOR APPLICATION NUMBER: PCT/US01/14349			
; PRIOR FILING DATE: 2001-05-02			
; PRIOR APPLICATION NUMBER: 09/563,222			
; PRIOR FILING DATE: 2000-05-02			
; NUMBER OF SEQ ID NOS: 182			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 114			
; LENGTH: 32			
; TYPE: PRT			
; ORGANISM: Mus musculus			
US-10-783-950-114			
Query Match			
Best Local Similarity 100.0%; Score 33; DB 17; Length 32;			
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 FTLKISR 7		
Db	15 FTLKISR 21		
RESULT 11			
US-09-905-243-61			
; Sequence 61, Application US/09905243			
; Patent No. US20020062009A1			
; GENERAL INFORMATION:			
; APPLICANT: Taylor, Alexander H			
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced			
; TITLE OF INVENTION: Immunogenicity			
; FILE REFERENCE: P50770			
; CURRENT APPLICATION NUMBER: US/09/905,243			
; CURRENT FILING DATE: 2001-07-16			
; PRIOR APPLICATION NUMBER: 09/300,970			
; PRIOR FILING DATE: 1999-04-28			
; NUMBER OF SEQ ID NOS: 97			
; SOFTWARE: FastSEQ for Windows Version 3.0			
; SEQ ID NO 61			
; LENGTH: 93			
; TYPE: PRT			
; ORGANISM: Macaca cynomolgus			
; FEATURE:			
; NAME/KEY: DOMAIN			
; LOCATION: (24)...(39)			
; OTHER INFORMATION: CDRI			
; NAME/KEY: DOMAIN			
; LOCATION: (54)...(61)			
; OTHER INFORMATION: CDRII			
US-09-905-243-61			
Query Match			
Best Local Similarity 100.0%; Score 33; DB 9; Length 93;			
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 FTLKISR 7		
Db	15 FTLKISR 21		
RESULT 12			
US-10-041-860-281			
; Sequence 281, Application US/10041860			
; Publication No. US20030157109A1			
; GENERAL INFORMATION:			
; APPLICANT: Corvalan, Jose R.F.			
; APPLICANT: Jia, Xiao-Chi			
; APPLICANT: Feng, Xiao			
; APPLICANT: Yang, Xiao-Dong			
; APPLICANT: Chen, Francine			
; APPLICANT: Gazit, Gadi			
; APPLICANT: Weber, Richard			
; APPLICANT: Bezabeh, Binyam			
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES			
; TITLE OF INVENTION: THEREOF			
; FILE REFERENCE: ABGENIX.051A			
; CURRENT APPLICATION NUMBER: US/10/041,860			
; CURRENT FILING DATE: 2002-01-07			
; NUMBER OF SEQ ID NOS: 377			
; SOFTWARE: FastSEQ for Windows Version 4.0			
; SEQ ID NO 281			
; LENGTH: 99			
; TYPE: PRT			
; ORGANISM: homo sapiens			
; FEATURE:			
; NAME/KEY: VARIANT			
; LOCATION: 31			
; OTHER INFORMATION: Xaa = Any Amino Acid			
; FEATURE:			
; NAME/KEY: VARIANT			
; LOCATION: 31			
; OTHER INFORMATION: Xaa = Any Amino Acid			
US-10-041-860-281			
Query Match			
Best Local Similarity 100.0%; Score 33; DB 14; Length 99;			
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 FTLKISR 7		
Db	76 FTLKISR 82		
RESULT 13			
US-10-041-860-323			
; Sequence 323, Application US/10041860			
; Publication No. US20030157109A1			
; GENERAL INFORMATION:			
; APPLICANT: Corvalan, Jose R.F.			
; APPLICANT: Jia, Xiao-Chi			
; APPLICANT: Feng, Xiao			
; APPLICANT: Yang, Xiao-Dong			
; APPLICANT: Chen, Francine			
; APPLICANT: Gazit, Gadi			
; APPLICANT: Weber, Richard			
; APPLICANT: Bezabeh, Binyam			
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES			
; TITLE OF INVENTION: THEREOF			
; FILE REFERENCE: ABGENIX.051A			
; CURRENT APPLICATION NUMBER: US/10/041,860			
; CURRENT FILING DATE: 2002-01-07			
; NUMBER OF SEQ ID NOS: 377			
; SOFTWARE: FastSEQ for Windows Version 4.0			
; SEQ ID NO 323			
; LENGTH: 99			
; TYPE: PRT			
; ORGANISM: homo sapiens			
US-10-041-860-323			
Query Match			
Best Local Similarity 100.0%; Score 33; DB 14; Length 99;			
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 FTLKISR 7		
Db	76 FTLKISR 82		

Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
| | | | |
Db 76 FTLKISR 82

Search completed: November 4, 2004, 07:03:46
Job time : 143 secs

RESULT 14
US-10-041-860-365
; Sequence 365, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 365
; LENGTH: 99
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 43, 58, 96
; OTHER INFORMATION: Xaa = Any Amino Acid
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 43, 58, 96
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-041-860-365

Query Match 100.0%; Score 33; DB 14; Length 99;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
| | | | |
Db 76 FTLKISR 82

RESULT 15
US-10-308-817-176
; Sequence 176, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 176
; LENGTH: 99
; TYPE: PRT
; ORGANISM: human
US-10-308-817-176

Query Match 100.0%; Score 33; DB 14; Length 99;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 01:09:51 ; Search time 23.6667 Seconds
(without alignments)
19.615 Million cell updates/sec

Title: US-09-712-819D-1
Perfect score: 32
Sequence: 1 FTLTISS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 58200

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	20	62.5	7	4	US-08-753-750B-20
2	18	56.2	7	3	US-09-187-859-637
3	18	56.2	7	4	US-09-839-542B-637
4	17	53.1	5	3	US-08-757-177-16
5	17	53.1	6	4	US-09-155-613A-59
6	17	53.1	6	4	US-09-266-805-5
7	17	53.1	6	4	US-09-530-139-14
8	17	53.1	7	2	US-08-739-401A-6
9	17	53.1	7	4	US-08-753-750B-19
10	16	50.0	4	3	US-08-860-904-9
11	16	50.0	4	4	US-09-301-593-47
12	16	50.0	6	1	US-08-252-995D-7
13	16	50.0	6	2	US-08-478-386A-46
14	16	50.0	6	2	US-08-292-597-46
15	16	50.0	6	2	US-08-388-653-46
16	16	50.0	6	2	US-08-473-985-46
17	16	50.0	6	2	US-08-834-108-7
18	16	50.0	6	2	US-08-483-898-46
19	16	50.0	6	3	US-09-087-716-46
20	16	50.0	6	3	US-09-157-753-46
21	16	50.0	6	3	US-09-157-230-46
22	16	50.0	6	3	US-09-087-811-46
23	16	50.0	6	3	US-09-156-855-46
24	16	50.0	6	3	US-09-158-010-46
25	16	50.0	6	3	US-09-087-647-46
26	16	50.0	6	3	US-09-302-629-46
27	16	50.0	7	1	US-08-136-743B-55

28	16	50.0	7	2	US-08-177-109A-7	Sequence 7, Appli
29	16	50.0	7	2	US-08-687-706-7	Sequence 7, Appli
30	16	50.0	7	3	US-09-040-216-28	Sequence 28, Appl
31	15	46.9	5	1	US-08-136-743B-63	Sequence 63, Appl
32	15	46.9	5	2	US-08-667-001-22	Sequence 22, Appl
33	15	46.9	5	3	US-09-040-216-55	Sequence 55, Appl
34	15	46.9	5	3	US-08-591-632-17	Sequence 17, Appl
35	15	46.9	5	3	US-08-591-632-23	Sequence 23, Appl
36	15	46.9	5	3	US-08-591-632-26	Sequence 26, Appl
37	15	46.9	5	3	US-09-611-451-17	Sequence 17, Appl
38	15	46.9	5	3	US-09-611-451-23	Sequence 23, Appl
39	15	46.9	5	3	US-09-611-451-26	Sequence 26, Appl
40	15	46.9	6	1	US-08-136-743B-62	Sequence 62, Appl
41	15	46.9	6	1	US-08-297-731-4	Sequence 4, Appli
42	15	46.9	6	1	US-08-290-448A-41	Sequence 41, Appl
43	15	46.9	6	1	US-08-290-448A-41	Sequence 41, Appl
44	15	46.9	6	1	US-08-175-069A-41	Sequence 41, Appl
45	15	46.9	6	2	US-08-622-720A-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-753-750B-20
; Sequence 20, Application US/08753750B
; Patent No. 6610506
; GENERAL INFORMATION:
; APPLICANT: Lo, Reggie Y.C.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Potter, Andrew A.
; TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF
; TITLE OF INVENTION: PASTEURILLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME
; FILE REFERENCE: A34762 021645.0105
; CURRENT APPLICATION NUMBER: US/08/753,750B
; CURRENT FILING DATE: 1996-11-29
; PRIOR APPLICATION NUMBER: CA 2,164,274
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 60/008,569
; PRIOR FILING DATE: 1995-12-01
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Escherichia coli
US-08-753-750B-20

Query Match 62.5%; Score 20; DB 4; Length 7;
Best Local Similarity 42.9%; Pred. No. 3.8e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTLTISS 7
Db 1 FTLSVDA 7

RESULT 2
US-09-187-859-637
; Sequence 637, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 10086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 637
; LENGTH: 7

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;
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-09-187-859-637

Query Match          56.2%; Score 18; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 FTLTISS 7
      ||: ||
Db      1 FTIDSSS 7

RESULT 3
US-09-839-542B-637
; Sequence 637, Application US/098339542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 637
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-09-839-542B-637

Query Match          56.2%; Score 18; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 FTLTISS 7
      ||: ||
Db      1 FTIDSSS 7

RESULT 4
US-08-757-177-16
; Sequence 16, Application US/08757177
; Patent No. 6071718
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, PRADIP
; APPLICANT: HARDS, ROBERT G.
; APPLICANT: THURMOND, JENNIFER M.
; APPLICANT: LEONARD, AMANDA FUN-YEONG
; TITLE OF INVENTION: METHODS OF PRODUCING A RECOMBINANT PROTEIN
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: One Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,177
; FILING DATE: 27-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6004.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 848-938-2623
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-757-177-16

Query Match          53.1%; Score 17; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 TISS 7
      ||||
Db      2 TISS 5

RESULT 5
US-09-155-613A-59
; Sequence 59, Application US/09155613A
; Patent No. 6420120
; GENERAL INFORMATION:
; APPLICANT: Boulanger, Pierre
; APPLICANT: Hong, Saw See
; APPLICANT: Karayan, Lucie
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
; FILE REFERENCE: 032751-036
; CURRENT APPLICATION NUMBER: US/09/155,613A
; CURRENT FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: PCT/FR98/00184
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: FR 97/01005
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: FR 97/11166
; PRIOR FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Phagotope
US-09-155-613A-59

Query Match          53.1%; Score 17; DB 4; Length 6;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLT 4
      :|||
Db      3 YTLT 6

RESULT 6
US-09-266-805-5
; Sequence 5, Application US/09266805
; Patent No. 6517829
; GENERAL INFORMATION:
; APPLICANT: Unilever N.V.
```

```
; APPLICANT: Unilever PLC
; TITLE OF INVENTION: New products comprising inactivated yeasts or moulds
; TITLE OF INVENTION: provided with active antibodies
; FILE REFERENCE: t-7055
; CURRENT APPLICATION NUMBER: US/09/266,805
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: llama
;
US-09-266-805-5

Query Match          53.1%; Score 17; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTISS 7
Db 2 VTVSS 6

RESULT 7
US-09-530-139-14
; Sequence 14, Application US/09530139
; Patent No. 6670453
; GENERAL INFORMATION:
; APPLICANT: FRENKEN, LEON GERARDUS
; APPLICANT: HOWELL, STEVEN
; APPLICANT: LEDEBOER, ADRIANUS MARINUS
; APPLICANT: VAN DER LOGT, CORNELIS PAUL
; TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS
; FILE REFERENCE: 60113/268075/ASH
; CURRENT APPLICATION NUMBER: US/09/530,139
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/EP98/06991
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: EP 97308538.4
; PRIOR FILING DATE: 1997-10-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-530-139-14

Query Match          53.1%; Score 17; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTISS 7
Db 2 VTVSS 6

RESULT 8
US-08-739-401A-6
; Sequence 6, Application US/08739401A
; Patent No. 5837461
; GENERAL INFORMATION:
; APPLICANT: Neitz, Maureen E.
; APPLICANT: Neitz, John F.
; TITLE OF INVENTION: DETECTION OF CONE-PHOTORECEPTOR-BASED
; TITLE OF INVENTION: VISION DISORDERS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
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; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,401A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 650053.91151
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5709
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-739-401A-6

Query Match          53.1%; Score 17; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTILT 4
Db 2 FTVT 5

RESULT 9
US-08-753-750B-19
; Sequence 19, Application US/08753750B
; Patent No. 6610506
; GENERAL INFORMATION:
; APPLICANT: Lo, Reggie Y.C.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Potter, Andrew A.
; TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF
; TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME
; FILE REFERENCE: A34762 021645.0105
; CURRENT APPLICATION NUMBER: US/08/753,750B
; CURRENT FILING DATE: 1996-11-29
; PRIOR APPLICATION NUMBER: CA 2,164,274
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 60/008,569
; PRIOR FILING DATE: 1995-12-01
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Escherichia coli
US-08-753-750B-19

Query Match          53.1%; Score 17; DB 4; Length 7;
Best Local Similarity 33.3%; Pred. No. 3.8e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLTISS 7
Db 2 TITVTA 7

RESULT 10
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US-08-860-904-9
; Sequence 9, Application US/08860904
; Patent No. 6294654
; GENERAL INFORMATION:
; APPLICANT: Sandlie, Inger
; APPLICANT: Bogen, Bjarne
; APPLICANT: Fossum, Sigbjorn
; TITLE OF INVENTION: A Modified Immunoglobulin Molecule
; TITLE OF INVENTION: Incorporating an Antigen in a No. 6294654-CDR
; TITLE OF INVENTION: Loop Region
; FILE REFERENCE: 9914-1
; CURRENT APPLICATION NUMBER: US/08/860,904
; CURRENT FILING DATE: 1997-09-29
; EARLIER APPLICATION NUMBER: PCT/GB96/00116
; EARLIER FILING DATE: 1996-01-19
; EARLIER APPLICATION NUMBER: GB 9501079.9
; EARLIER FILING DATE: 1995-01-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Mus sp.
US-08-860-904-9

Query Match 50.0%; Score 16; DB 3; Length 4;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TISS 7
|:|
Db 1 TVSS 4

RESULT 11

US-09-301-593-47
; Sequence 47, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-47

Query Match 50.0%; Score 16; DB 4; Length 4;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TISS 7
|:|
Db 1 TVSS 4

RESULT 12

US-08-252-995D-7
; Sequence 7, Application US/08252995D

Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3V2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-252-995D-7

Query Match 50.0%; Score 16; DB 1; Length 6;
Best Local Similarity 60.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTISS 7
|:|
Db 2 LTLSN 6

RESULT 13

US-08-478-386A-46
; Sequence 46, Application US/08478386A
; Patent No. 5830462
; GENERAL INFORMATION:
; APPLICANT: Crabtree, Gerald R.
; APPLICANT: Schreiber, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Wandless, Thomas J.
; APPLICANT: Belshaw, Peter
; TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED
; TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Landsdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC/DOS/MS/DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,386A
; FILING DATE: 07/JUN/1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Figg, E. Anthony
; REGISTRATION NUMBER: 27,195
; REFERENCE/DOCKET NUMBER: 2054-114A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-478-386A-46

Query Match          50.0%; Score 16; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 LTIS 6
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Db      3 LTVS 6

RESULT 14
US-08-292-597-46
; Sequence 46, Application US/08292597
; Patent No. 5834266
; GENERAL INFORMATION:
; APPLICANT: Gerald R. Crabtree
; APPLICANT: Schreiber, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Wandless, Thomas J.
; APPLICANT: Belshaw, Peter
; TITLE OF INVENTION: Regulated Apoptosis
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Landsdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC/DOS/MS/DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,597
; FILING DATE: 18/AUG/1994
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Figg, E. Anthony
; REGISTRATION NUMBER: 27,195
; REFERENCE/DOCKET NUMBER: 2054-108A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
US-08-292-597-46

Query Match          50.0%; Score 16; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 LTIS 6
      ||:|
Db      3 LTVS 6

RESULT 15
US-08-388-653-46
; Sequence 46, Application US/08388653
; Patent No. 5869337
; GENERAL INFORMATION:
; APPLICANT: Crabtree, Gerald R.
; APPLICANT: Schreiber, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Wandless, Thomas J.
; APPLICANT: Belshaw, Peter
; TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED
; TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Landsdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC/DOS/MS/DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,653
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 08/478,386
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Figg, E. Anthony
; REGISTRATION NUMBER: 27,195
; REFERENCE/DOCKET NUMBER: 2054-114A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-388-653-46

Query Match          50.0%; Score 16; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 LTIS 6
      ||:|
Db      3 LTVS 6

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OM protein - protein search, using sw model

Run on: November 4, 2004, 01:23:27 ; Search time 69.3333 Seconds
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Title: US-09-712-819D-1
Perfect score: 32
Sequence: 1 FTLTSS 7

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Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 56143

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	22	68.8	6	14	US-10-150-654A-18
2	18	56.2	7	14	US-10-006-869-637
3	18	56.2	7	14	US-10-349-507-11
4	18	56.2	7	14	US-10-267-565-11
5	18	56.2	7	14	US-10-395-032-637
6	17	53.1	5	10	US-09-788-006-107
7	17	53.1	5	10	US-09-788-006-108
8	17	53.1	5	14	US-10-154-971-29
9	17	53.1	5	16	US-10-803-622-2
10	17	53.1	5	16	US-10-803-653-2
11	17	53.1	6	9	US-09-777-921A-17
12	17	53.1	6	10	US-09-530-139-14
13	17	53.1	6	13	US-10-156-820-59

14	17	53.1	6	14	US-10-097-175-97	Sequence 97, Appl
15	17	53.1	6	15	US-10-698-489-17	Sequence 17, Appl
16	16	50.0	4	9	US-09-301-593-47	Sequence 47, Appl
17	16	50.0	4	14	US-10-159-006-47	Sequence 47, Appl
18	16	50.0	6	14	US-10-020-354-102	Sequence 102, App
19	16	50.0	6	15	US-10-054-712-46	Sequence 46, Appl
20	16	50.0	6	17	US-10-699-088-519	Sequence 519, App
21	16	50.0	7	9	US-09-832-723-69	Sequence 69, Appl
22	16	50.0	7	9	US-09-996-288-164	Sequence 164, App
23	16	50.0	7	10	US-09-996-265-164	Sequence 164, App
24	16	50.0	7	14	US-10-303-331-69	Sequence 69, Appl
25	16	50.0	7	14	US-10-022-066-214	Sequence 214, App
26	16	50.0	7	15	US-10-461-863-164	Sequence 164, App
27	15	46.9	5	14	US-10-286-186-3	Sequence 3, Appli
28	15	46.9	5	14	US-10-286-186-4	Sequence 4, Appli
29	15	46.9	5	14	US-10-315-964A-394	Sequence 394, App
30	15	46.9	5	14	US-10-317-251A-394	Sequence 394, App
31	15	46.9	5	14	US-10-317-252A-394	Sequence 394, App
32	15	46.9	6	9	US-09-876-388-6	Sequence 6, Appli
33	15	46.9	6	14	US-10-105-930-39	Sequence 39, Appl
34	15	46.9	6	14	US-10-006-869-650	Sequence 650, App
35	15	46.9	6	14	US-10-287-892-6	Sequence 6, Appli
36	15	46.9	6	14	US-10-288-340-6	Sequence 6, Appli
37	15	46.9	6	14	US-10-315-964A-402	Sequence 402, App
38	15	46.9	6	14	US-10-317-251A-402	Sequence 402, App
39	15	46.9	6	14	US-10-317-252A-402	Sequence 402, App
40	15	46.9	6	14	US-10-395-032-650	Sequence 650, App
41	15	46.9	6	15	US-10-394-980-243	Sequence 243, App
42	15	46.9	6	15	US-10-418-972-55	Sequence 55, Appl
43	15	46.9	6	15	US-10-374-466-47	Sequence 47, Appl
44	15	46.9	6	16	US-10-722-733-6	Sequence 6, Appli
45	15	46.9	6	16	US-10-723-099-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-10-150-654A-18
; Sequence 18, Application US/10150654A
; Publication No. US20030198595A1
; GENERAL INFORMATION:
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: HANSEN, HANS J.
; APPLICANT: LEUNG, SHUI-ON
; APPLICANT: MCBRIDE, WILLIAM J.
; APPLICANT: QU, ZHENGXING
; TITLE OF INVENTION: PRODUCTION AND USE OF NOVEL PEPTIDE-BASED AGENTS FOR
; FILE REFERENCE: 018733-1085
; CURRENT APPLICATION NUMBER: US/10/150,654A
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/382,186
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 09/823,746
; PRIOR FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-150-654A-18

Query Match 68.8%; Score 22; DB 14; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TLTISS 7
|:|:|

Db 1 TVTVSS 6

RESULT 2
US-10-006-869-637
; Sequence 637, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 637
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-10-006-869-637

Query Match 56.2%; Score 18; DB 14; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTLTVSS 7
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Db 1 FTIDSSS 7

RESULT 3
US-10-349-507-11
; Sequence 11, Application US/10349507
; Publication No. US20030199002A1
; GENERAL INFORMATION:
; APPLICANT: Hekimi, Siegfried
; APPLICANT: Jiang, Ning
; APPLICANT: Benard, Claire
; APPLICANT: Kebir, Hania
; APPLICANT: McCright, Brenton
; APPLICANT: Lakowski, Bernard
; TITLE OF INVENTION: CLK-2 NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: 11202-006-999
; CURRENT APPLICATION NUMBER: US/10/349,507
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 10/312,187
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: PCT/CA01/00913
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/213,174
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/254,932
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-349-507-11

Query Match 56.2%; Score 18; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLTI 5

Db 1 TLTI 4

RESULT 4
US-10-267-565-11
; Sequence 11, Application US/10267565
; Publication No. US20030204059A1
; GENERAL INFORMATION:
; APPLICANT: Gately, Maurice
; APPLICANT: Gubler, Ulrich
; APPLICANT: Hulmes, Jeffery
; APPLICANT: Podlaski, Frank
; APPLICANT: Stern, Alvin
; TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF CYTOTOXIC
; TITLE OF INVENTION: LYMPHOCYTE MATURATION FACTOR AND MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES THERETO
; FILE REFERENCE: 11126-005
; CURRENT APPLICATION NUMBER: US/10/267,565
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: 09/401,839
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 08/459,151
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 08/205,011
; PRIOR FILING DATE: 1994-03-02
; PRIOR APPLICATION NUMBER: 07/857,023
; PRIOR FILING DATE: 1992-03-24
; PRIOR APPLICATION NUMBER: 07/572,284
; PRIOR FILING DATE: 1990-08-27
; PRIOR APPLICATION NUMBER: 07/520,935
; PRIOR FILING DATE: 1990-05-09
; PRIOR APPLICATION NUMBER: 07/455,708
; PRIOR FILING DATE: 1989-12-22
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-565-11

Query Match 56.2%; Score 18; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLTI 5
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Db 1 TLTI 4

RESULT 5
US-10-395-032-637
; Sequence 637, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 637
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion


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; OTHER INFORMATION: recognition sequence
US-10-395-032-637

Query Match      56.2%; Score 18; DB 14; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 FTLTSS 7
      ||: ||
Db      1 FTIDSS 7

RESULT 6
US-09-788-006-107
; Sequence 107, Application US/09788006
; Publication No. US20030036093A1
; GENERAL INFORMATION:
; APPLICANT: Floudas, Christopher A.
; APPLICANT: Klepeis, John L.
; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and
; TITLE OF INVENTION: Polypeptide Tertiary Structures
; FILE REFERENCE: PU-0007
; CURRENT APPLICATION NUMBER: US/09/788,006
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Streptomyces griseus
US-09-788-006-107

Query Match      53.1%; Score 17; DB 10; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLT 4
      ||: ||
Db      2 FTVT 5

RESULT 7
US-09-788-006-108
; Sequence 108, Application US/09788006
; Publication No. US20030036093A1
; GENERAL INFORMATION:
; APPLICANT: Floudas, Christopher A.
; APPLICANT: Klepeis, John L.
; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and
; TITLE OF INVENTION: Polypeptide Tertiary Structures
; FILE REFERENCE: PU-0007
; CURRENT APPLICATION NUMBER: US/09/788,006
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 108
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Streptomyces griseus
US-09-788-006-108

Query Match      53.1%; Score 17; DB 10; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLT 4
      ||: ||
Db      1 FTVT 4

RESULT 8
US-10-154-971-29
; Sequence 29, Application US/10154971
; Publication No. US20030088074A1
; GENERAL INFORMATION:
; APPLICANT: Hamers, Raymond
; APPLICANT: Muyldermans, Serge
; TITLE OF INVENTION: VARIABLE FRAGMENTS OF IMMUNOGLOBULINS -
; TITLE OF INVENTION: USE FOR THERAPEUTIC OR VETERINARY PURPOSES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENCER & FRANK
; STREET: 1100 New York Avenue, N.W., Suite 300 East
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/154,971
; FILING DATE: 28-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/945,244
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/EP96/01725
; FILING DATE: 25-APR-1996
; APPLICATION NUMBER: EP 95400932.0
; FILING DATE: 25-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gollin, Michael A.
; REGISTRATION NUMBER: 31,957
; REFERENCE/DOCKET NUMBER: GUPLA 0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-414-4000
; TELEFAX: 202-414-4040
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-154-971-29

Query Match      53.1%; Score 17; DB 14; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 LTISS 7
      :||: ||
Db      1 VTVSS 5

RESULT 9
US-10-803-622-2
; Sequence 2, Application US/10803622
; Publication No. US20040157214A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Ronald
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
```

```
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,622
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Bacteriophage fd
US-10-803-622-2

Query Match      53.1%; Score 17; DB 16; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 LTISS 7
      :|||
Db      1 VTVSS 5

RESULT 10
US-10-803-653-2
; Sequence 2, Application US/10803653
; Publication No. US20040157215A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,653
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
```

```
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Bacteriophage fd
US-10-803-653-2

Query Match      53.1%; Score 17; DB 16; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 LTISS 7
      :|||
Db      1 VTVSS 5

RESULT 11
US-09-777-921A-17
; Sequence 17, Application US/09777921A
; Patent No. US20020115136A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001103
; CURRENT APPLICATION NUMBER: US/09/777,921A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-777-921A-17

Query Match      53.1%; Score 17; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 LTISS 6
      :|||
Db      2 LTISS 5

RESULT 12
US-09-530-139-14
; Sequence 14, Application US/09530139
; Publication No. US20030092892A1
; GENERAL INFORMATION:
; APPLICANT: FRENKEN, LEON GERARDUS
; APPLICANT: HOWELL, STEVEN
; APPLICANT: LEDEBOER, ADRIANUS MARINUS
; APPLICANT: VAN DER LOGT, CORNELIS PAUL
; TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS
; FILE REFERENCE: 60113/268075/ASH
; CURRENT APPLICATION NUMBER: US/09/530,139
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/EP98/06991
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: EP 97308538.4
```

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; PRIOR FILING DATE: 1997-10-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-530-139-14
```

```
Query Match          53.1%; Score 17; DB 10; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 LTISS 7
       :|||
Db      2 VTVSS 6
```

```
RESULT 13
US-10-156-820-59
; Sequence 59, Application US/10156820
; Publication No. US20020150558A1
; GENERAL INFORMATION:
; APPLICANT: Boulanger, Pierre
; APPLICANT: Hong, Saw See
; APPLICANT: Karayan, Lucie
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
; FILE REFERENCE: 032751-036
; CURRENT APPLICATION NUMBER: US/10/156,820
; CURRENT FILING DATE: 2002-06-30
; PRIOR APPLICATION NUMBER: PCT/FR98/00184
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: FR 97/01005
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: FR 97/11166
; PRIOR FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Phagotopoe
US-10-156-820-59
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Query Match          53.1%; Score 17; DB 13; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

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QY      1 FTILT 4
       :|||
Db      3 YTLT 6
```

```
RESULT 14
US-10-097-175-97
; Sequence 97, Application US/10097175
; Publication No. US20030045680A1
; GENERAL INFORMATION:
; APPLICANT: JOYAL, JOHN L.
; APPLICANT: MUELLER, JOHN
; APPLICANT: OZA, VIBHA B.
; APPLICANT: FINDEIS, MARK A.
; TITLE OF INVENTION: PEPTIDIC MODULATORS OF THE ANDROGEN RECEPTOR
; FILE REFERENCE: PPI-110
; CURRENT APPLICATION NUMBER: US/10/097,175
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/275,240
; PRIOR FILING DATE: 2001-03-12
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; PRIOR APPLICATION NUMBER: 60/352,399
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Androgen Receptor Binding Polypeptides
US-10-097-175-97
```

```
Query Match          53.1%; Score 17; DB 14; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      3 LTISS 7
       :|||
Db      1 LTIES 5
```

```
RESULT 15
US-10-698-489-17
; Sequence 17, Application US/10698489
; Publication No. US20040067523A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001103CON
; CURRENT APPLICATION NUMBER: US/10/698,489
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: To Be Assigned
; PRIOR FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: 09/777,921
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-698-489-17
```

```
Query Match          53.1%; Score 17; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 LTIS 6
       :|||
Db      2 LTIS 5
```

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Search completed: November 4, 2004, 01:43:16
Job time : 70.6667 secs
```

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 4, 2004, 01:09:31 ; Search time 18.3333 Seconds
(without alignments)
36.737 Million cell updates/sec

Title: US-09-712-819D-1
Perfect score: 32
Sequence: 1 FTLTSS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	11	34.4	4	2 A40135	branched-chain-ami
2	11	34.4	5	2 B44817	34.5K structural p
3	11	34.4	5	2 D44817	35K structural pro
4	11	34.4	5	2 PT0644	T-cell receptor be
5	10	31.2	7	2 E30608	Ig kappa chain V-I
6	9	28.1	3	3 T13892	cytochrome-c oxida
7	9	28.1	5	2 E60274	major protein anti
8	9	28.1	5	2 A37114	hypoxanthine phosph
9	9	28.1	5	2 H44817	34.5K structural p
10	9	28.1	5	2 F44817	34.5K structural p
11	9	28.1	5	2 S69237	surface protein te
12	9	28.1	5	2 E42364	flagellar protein
13	9	28.1	6	2 A60986	N-formyl oligopept
14	9	28.1	6	2 S14159	paraspinal crystal
15	9	28.1	6	2 A43766	28K ubiquitin-immu
16	9	28.1	6	2 I37263	Y protein - human
17	9	28.1	6	2 I65546	MHC H2-L antigen -
18	9	28.1	7	2 S25266	pile protein - Esc
19	9	28.1	7	2 PS0254	18K protein 5507 -
20	9	28.1	7	2 PN0649	pullulanase (EC 3.
21	9	28.1	7	2 S09066	globulin IV alpha
22	9	28.1	7	2 A25269	sex pheromone cAM3
23	9	28.1	7	2 A30812	sex pheromone cCF1
24	8	25.0	3	3 PT0622	T-cell receptor be
25	8	25.0	4	2 PT0696	T-cell receptor be
26	8	25.0	4	2 PT0645	T-cell receptor be
27	8	25.0	4	2 PT0712	T-cell receptor be
28	8	25.0	4	2 PT0698	T-cell receptor be
29	8	25.0	4	2 PT0551	T-cell receptor be

30	8	25.0	4	2 PT0697	T-cell receptor be
31	8	25.0	5	2 I39964	ribosomal protein
32	8	25.0	5	2 I39966	ribosomal protein
33	8	25.0	5	2 I39965	ribosomal protein
34	8	25.0	5	2 T10954	hypothetical prote
35	8	25.0	5	2 I50385	myosin light chain
36	8	25.0	5	2 PT0308	Ig heavy chain CRD
37	8	25.0	5	2 PT0596	T-cell receptor be
38	8	25.0	5	2 PT0610	T-cell receptor be
39	8	25.0	5	2 PT0597	T-cell receptor be
40	8	25.0	5	2 PT0729	T-cell receptor be
41	8	25.0	5	2 PT0624	T-cell receptor be
42	8	25.0	5	2 PT0625	T-cell receptor be
43	8	25.0	5	2 PT0672	T-cell receptor be
44	8	25.0	5	2 PT0660	T-cell receptor be
45	8	25.0	5	2 PT0656	T-cell receptor be

ALIGNMENTS

RESULT 1

A40135
branched-chain-amino-acid transaminase (EC 2.6.1.42), mitochondrial - rat (fragment)
N;Alternate names: branched-chain-amino-acid aminotransferase, mitochondrial
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-May-1992 #sequence_revision 13-May-1992 #text_change 30-Sep-1993
C;Accession: A40135
R;Hutson, S.M.; Wallin, R.; Hall, T.R.
submitted to the Protein Sequence Database, March 1992
A;Reference number: A40135
A;Accession: A40135
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-4 <HUT>
C;Keywords: aminotransferase; mitochondrion

Query Match 34.4%; Score 11; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISS 7
Db 1 VSS 3

RESULT 2

B44817
34.5K structural protein - Leuconostoc oenos phage PZt11-15 (fragment)
C;Species: Leuconostoc oenos phage PZt11-15
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: B44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: B44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70342)

Query Match 34.4%; Score 11; DB 2; Length 5;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LTISS 7
Db 1 LATSS 5

RESULT 3

D44817
35K structural protein - Leuconostoc oenos phage PAT5-12 (fragment)

C;Species: Leuconostoc oenos phage PAT5-12
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: D44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: D44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70340)

Query Match 34.4%; Score 11; DB 2; Length 5;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LTISS 7
Db 1 LATSS 5

RESULT 4
PT0644
T-cell receptor beta chain V-D-J region (111-1G) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: PT0644
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0644
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Cross-references: UNIPROT:Q9Z2T6
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 34.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2
Db 4 FT 5

RESULT 5
E30608
Ig kappa chain V-III region (Gag) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996
C;Accession: E30608
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Soldo
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies.
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: E30608
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <GON>
C;Keywords: heterotetramer; immunoglobulin

Query Match 31.2%; Score 10; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LTIS 6
Db 4 LTQS 7

RESULT 6
T13892
cytochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrion (fragment)
C;Species: mitochondrion Lampetra fluviatilis (river lamprey)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: T13892
R;Delarbre, C.; Barriol, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol. 14, 807-813, 1997
A;Title: The main features of the cranial mitochondrial DNA between the ND1 and the COII
A;Reference number: Z17775; MUID:97398704; PMID:9254918
A;Accession: T13892
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-3
A;Cross-references: EMBL:Y09528; NID:G2340016; PIDN:CAA70721.1; PID:G4379123
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match 28.1%; Score 9; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
Db 2 TL 3

RESULT 7
E60274
major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)
C;Species: Mycobacterium tuberculosis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C;Accession: E60274
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A;Title: Isolation and partial characterization of major protein antigens in the culture supernatant of Mycobacterium tuberculosis.
A;Reference number: A60274; MUID:91099989; PMID:1898899
A;Accession: E60274
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <NAG>

Query Match 28.1%; Score 9; DB 2; Length 5;
Best Local Similarity 25.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLT 4
Db 2 YPIT 5

RESULT 8
A37114
hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - fluke (Schistosoma mansoni) (fragment)
C;Species: Schistosoma mansoni
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 23-Jun-1993
C;Accession: A37114
R;Yuan, L.; Craig, S.P.; McKerrow, J.H.; Wang, C.C.
J. Biol. Chem. 265, 13528-13532, 1990
A;Title: The hypoxanthine-guanine phosphoribosyltransferase of Schistosoma mansoni.
A;Reference number: A37114; MUID:90337955; PMID:2199439
A;Accession: A37114
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <YUA>
C;Keywords: glycosyltransferase; pentosyltransferase

Query Match 28.1%; Score 9; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ISS 7
: ||
Db 1 MSS 3

RESULT 9

H44817

34.5K structural protein - Leuconostoc oenos phase P32 (fragment)

C;Species: Leuconostoc oenos phase P32

C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998

C;Accession: H44817

R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991

A;Title: Lysogeny in Leuconostoc oenos.

A;Reference number: A44817; MUID:92085033; PMID:1748868

A;Accession: H44817

A;Molecule type: protein

A;Residues: 1-5 <ARE>

A;Note: sequence extracted from NCBI backbone (NCBIP:70332)

Query Match 28.1%; Score 9; DB 2; Length 5;

Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LTISS 7

: |||

Db 1 MATSS 5

RESULT 10

F44817

34.5K structural protein - Leuconostoc oenos phase P54 (fragment)

C;Species: Leuconostoc oenos phase P54

C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998

C;Accession: F44817

R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991

A;Title: Lysogeny in Leuconostoc oenos.

A;Reference number: A44817; MUID:92085033; PMID:1748868

A;Accession: F44817

A;Molecule type: protein

A;Residues: 1-5 <ARE>

A;Note: sequence extracted from NCBI backbone (NCBIP:70335)

Query Match

28.1%; Score 9; DB 2; Length 5;

Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LTISS 7

: |||

Db 1 MATSS 5

RESULT 11

S69237

surface protein tetrabrachion heavy chain - Staphylothermus marinus (fragment)

C;Species: Staphylothermus marinus

C;Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 17-Mar-1999

C;Accession: S69237

R;Peters, J.; Nitsch, M.; Kuehlmoorgen, B.; Golbik, R.; Lupas, A.; Kellermann, J.; Engelh

J. Mol. Biol. 245, 385-401, 1995

A;Title: Tetrabrachion: a filamentous archaeobacterial surface protein assembly of unusua

A;Reference number: S69237; MUID:95139068; PMID:7837271

A;Accession: S69237

A;Molecule type: protein

A;Residues: 1-5 <PET>

A;Experimental source: strain F1, DSM 3639

C;Keywords: cell wall; glycoprotein; heat-stable protein

Query Match

28.1%; Score 9; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TL 3
: ||
Db 2 TL 3

RESULT 12

E42364

flagellar protein flir - Salmonella typhimurium (fragment)

C;Species: Salmonella typhimurium

C;Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 09-Jul-2004

C;Accession: E42364

R;Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.

J. Bacteriol. 173, 3564-3572, 1991

A;Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and s

A;Reference number: A42364; MUID:91258342; PMID:1646201

A;Accession: E42364

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-5 <VOG>

A;Cross-references: UNIPROT:P26416; GB:M62408

Query Match

28.1%; Score 9; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TL 3

: ||

Db 3 TL 4

RESULT 13

A60986

N-formyl oligopeptide - Escherichia coli (fragment)

C;Species: Escherichia coli

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993

C;Accession: A60986

R;Broom, M.F.; Mellor, D.M.; Chadwick, V.S.

Experientia 45, 1097-1099, 1989

A;Title: Purification and amino acid sequencing of naturally occurring N-formyl-methion

A;Reference number: A60986; MUID:90092408; PMID:2689204

A;Accession: A60986

A;Molecule type: protein

A;Residues: 1-6 <BRO>

C;Comment: This hexapeptide was the longest of several N-formyl oligopeptides reported.

F;1/Modified site: N-formylmethionine #status experimental

Query Match

28.1%; Score 9; DB 2; Length 6;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTL 3

: ||

Db 3 FIL 5

RESULT 14

S14159

parasporal crystal protein CryIC - Bacillus thuringiensis (fragment)

N;Alternate names: delta-endotoxin

C;Species: Bacillus thuringiensis

C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 18-Jul-1997

C;Accession: S14159

R;Convents, D.; Cherlet, M.; van Damme, J.; Lasters, I.; Lauwereys, M.

Eur. J. Biochem. 195, 631-635, 1991

A;Title: Two structural domains as a general fold of the toxic fragment of the Bacillus

A;Reference number: S14087; MUID:91153300; PMID:1847865

A;Accession: S14159

A;Molecule type: protein

A;Residues: 1-6 <CON>

Query Match

28.1%; Score 9; DB 2; Length 6;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISS 7
||:
Db 1 IST 3

RESULT 15
A43766
28K ubiquitin-immunoreactive protein - inky cap (Coprinus cinereus) (fragment)
C:Species: Coprinus cinereus
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 30-Sep-1993
C:Accession: A43766
R;Kanda, T.; Inoue, M.; Akiyama, M.
Biochimie 72, 355-359, 1990
A:Title: Purification and characterization of an ubiquitin-immuno-reactive protein local
A:Reference number: A43766; MUID:91002724; PMID:1698461
A:Accession: A43766
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-6 <KAN>

Query Match 28.1%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
||
Db 5 TL 6

Search completed: November 4, 2004, 01:24:17
Job time : 18.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:55:00 ; Search time 99.6667 Seconds
(without alignments)
40.411 Million cell updates/sec

Title: US-09-712-819D-1
Perfect score: 32
Sequence: 1 FTLTSS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 167

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	16	50.0	7	2 P70804	P70804 azotobacter
2	12	37.5	7	1 GFRP MOUSE	P99025 mus musculus
3	12	37.5	7	2 O34028	O34028 sphingomona
4	11	34.4	5	1 RE31_LITRU	P82072 litoria rub
5	11	34.4	5	1 RE32_LITRU	P82073 litoria rub
6	11	34.4	7	2 P83530	P83530 lactobacill
7	11	34.4	7	2 Q54248	Q54248 streptomyce
8	10	31.2	5	1 E104_LITRU	P82100 litoria rub
9	10	31.2	6	2 P83533	P83533 lactobacill
10	9	28.1	7	1 CCF1_ENTFA	P20104 enterococcu
11	9	28.1	7	1 CIA_ENTFA	P11932 enterococcu
12	9	28.1	7	2 P82445	P82445 nicotiana t
13	9	28.1	7	2 O07354	O07354 synechococc
14	9	28.1	7	2 Q8JE81	Q8JE81 human immun
15	8	25.0	5	1 ALL4_CARMA	P81817 carcinus ma
16	8	25.0	5	1 BIOB_CITFR	P12997 citrobacter
17	8	25.0	5	1 PSK_DAUCA	P58261 daucus caro
18	8	25.0	6	1 LOK1_LOCMI	P41491 locusta mig
19	8	25.0	6	2 P82181	P82181 spinacia ol
20	8	25.0	6	2 P82182	P82182 spinacia ol
21	8	25.0	7	1 ALL2_CARMA	P81805 carcinus ma
22	8	25.0	7	1 ALL3_CARMA	P81806 carcinus ma
23	8	25.0	7	1 ALL4_CARMA	P81807 carcinus ma
24	8	25.0	7	1 ALL5_CARMA	P81808 carcinus ma
25	8	25.0	7	1 ALL7_CYPDPO	P82158 cydia pomon
26	8	25.0	7	1 UC24_MAIZE	P80630 zea mays (m
27	8	25.0	7	2 Q8TAQ4	Q8TAQ4 homo sapien
28	8	25.0	7	2 P72081	P72081 nocardia la
29	7	21.9	4	1 E0SI_HUMAN	P02731 homo sapien
30	7	21.9	4	1 YLM1_YEAST	P36515 saccharomyc
31	7	21.9	5	1 BIOA_CITFR	P13071 citrobacter

32	7	21.9	6	1 UN06_CLOPA	P81351 clostridium
33	7	21.9	7	2 P83492	P83492 bionectria
34	7	21.9	7	2 Q47029	Q47029 enterobacte
35	7	21.9	7	2 Q65578	Q65578 bovine herp
36	6	18.8	4	1 ACH1_ACHFU	P35904 achatina fu
37	6	18.8	4	1 FAR3_HIRME	P42562 hirudo medi
38	6	18.8	4	1 FAR4_HIRME	P42563 hirudo medi
39	6	18.8	4	1 FFKA_ANTEL	P58705 anthopleura
40	6	18.8	4	1 FLRF_HIRME	P42561 hirudo medi
41	6	18.8	4	1 FLRN_ANTEL	P58707 anthopleura
42	6	18.8	4	1 FMRF_MACNI	P01162 macrocallis
43	6	18.8	4	1 FYRI_OCTMI	P58706 anthopleura
44	6	18.8	4	1 OCPI_OCTMI	P58648 octopus min
45	6	18.8	4	2 Q16047	Q16047 homo sapien

ALIGNMENTS

RESULT 1
P70804

ID P70804 PRELIMINARY; PRT; 7 AA.
AC P70804;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Algt protein (Fragment).
GN Name=algt;
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E;
RX MEDLINE=96427318; PubMed=8830682;
RA Rehm B.H.A., Ertesvag H., Valla S.;
RT "A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is
RT part of an alg gene cluster physically organized in a manner similar
RT to that in Pseudomonas aeruginosa.";
RL J. Bacteriol. 178:5884-5889(1996).
DR EMBL; X87973; CAA61230.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 684 MW; 71B5A5A5A2D1AED0 CRC64;

Query Match 50.0%; Score 16; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TISS 7
Db 2 TVSS 5

RESULT 2

GFRP MOUSE
ID GFRP MOUSE STANDARD; PRT; 7 AA.
AC P99025;

DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).
GN Name=Gchfr; Synonyms=Gfrp;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.

RC TISSUE=Liver;
RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,
RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F., Cowthorne M.;
Submitted (AUG-1998) to Swiss-Prot.

```
CC -!- FUNCTION: Mediates tetrahydrobiopterin inhibition of GTP
CC cyclohydrolase I. This inhibition is reversed by L-phenylalanine
CC (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC SWISS-2DPAGE; P99025; MOUSE.
KW Direct protein sequencing.
FT INIT_MET 0 7
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 806 MW; 71B5B057273B4700 CRC64;

Query Match 37.5%; Score 12; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LTISS 7
Db 3 LLIST 7

RESULT 3
O34028 PRELIMINARY; PRT; 7 AA.
AC O34028;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Catechol-2,3-dioxygenase (Fragment).
GN Name=phnE;
OS Sphingomonas chungbukensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Sphingomonas.
OX NCBI_TaxID=56193;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DJ77;
RA Kim Y.-C.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88298; AAB66311.1; -.
DR GO; GO:0016702; F:oxidoreductase activity, acting on single d. . .; IEA.
KW Dioxygenase.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 868 MW; 71A452D1A699D460 CRC64;

Query Match 37.5%; Score 12; DB 2; Length 7;
Best Local Similarity 20.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTISS 7
Db 3 MTVNT 7

RESULT 4
RE31_LITRU STANDARD; PRT; 5 AA.
AC P82072;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
```

```
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAB; RANGE=1-5; NOTE=Ref.1.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
FT MOD_RES 5 5
FT SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 34.4%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2
Db 4 FT 5

RESULT 5
RE32_LITRU STANDARD; PRT; 5 AA.
ID RE32_LITRU
AC P82073;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rubellidin 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
KW Amphibian defense peptide; Direct protein sequencing.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 34.4%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2
Db 4 FT 5

RESULT 6
P83530 PRELIMINARY; PRT; 7 AA.
ID P83530
AC P83530;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Unknown protein from 2D-page (fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 20451;
RX PubMed=12112860;
RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
```

```

RT "High pressure effects step-wise altered protein expression in
RL Lactobacillus sanfranciscensis.";
RL Proteomics 2:765-774(2002).
CC -!- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
CC protein is: 15 kDa.
FT NON_TER 1 1
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 790 MW; 6AAB02CAA731B2A0 CRC64;

Query Match 34.4%; Score 11; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLT 5
Db 2 TLDV 5

RESULT 7
Q54248 PRELIMINARY; PRT; 7 AA.
AC Q54248;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE RplO protein (Fragment).
GN Name=rplO;
OS Streptomyces griseus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2-3-11;
RX MEDLINE=20011291; PubMed=10542330;
RA Poehling S., Piepersberg W., Wehmeier U.F.;
RT "Analysis and regulation of the sec Y gene from Streptomyces griseus
RT N2-3-11 and interaction of the SecY protein with the SecA protein.";
RL Biochim. Biophys. Acta 1447:298-302(1999).
DR EMBL; X95915; CAA65160.1; -.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 760 MW; 72C72B01B2D1B2A0 CRC64;

Query Match 34.4%; Score 11; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLT 4
Db 2 TVT 4

RESULT 8
EI04_LITRU STANDARD; PRT; 5 AA.
AC P82100;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Electrin 4.
OS Litoria rubella (desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).

```

```

CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
FT MOD_RES 5 5 Histidine amide.
SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

```

```

Query Match 31.2%; Score 10; DB 1; Length 5;
Best Local Similarity 33.3%; Pred. No. 1.8e+06;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 LTI 5
Db 2 ITV 4

```

RESULT 9

```

P83533 PRELIMINARY; PRT; 6 AA.
ID P83533;
AC P83533;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 20451;
RX PubMed=12112860;
RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
RT "High pressure effects step-wise altered protein expression in
RT Lactobacillus sanfranciscensis.";
RL Proteomics 2:765-774(2002).
CC -!- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
CC protein is: 15 kDa.
FT NON_TER 1 1
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 590 MW; 6DDDD452D1AAC000 CRC64;

```

```

Query Match 31.2%; Score 10; DB 2; Length 6;
Best Local Similarity 25.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY 4 TISS 7
Db 2 TVNA 5

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RESULT 10

```

CCF1_ENTFA STANDARD; PRT; 7 AA.
ID CCF1_ENTFA
AC P20104;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sex pheromone cCF10.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RA MEDLINE=89008313; PubMed=3139658;
RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.;
RA Adsit J.C., Dunny G.M., Suzuki A.;
RT "Structure of cCF10, a peptide sex pheromone which induces conjugative
RT transfer of the Streptococcus faecalis tetracycline resistance
RT plasmid, pCF10.";
RL J. Biol. Chem. 263:14574-14578(1988).
CC -!- FUNCTION: cCF10 is involved in the conjugative transfer of the
CC hemolysin plasmid pCF10.
DR PIR; A30812; A30812.

```

KW Direct protein sequencing; Pheromone.
SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;
Query Match 28.1%; Score 9; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TL 3
Db 3 TL 4
RESULT 11
CIA_ENTFA STANDARD; PRT; 7 AA.
AC P11932;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sex pheromone cAM373 (Clumping-inducing agent) (CIA).
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=87005252; PubMed=3033276;
RA Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
RA White B.A., An F.Y., Clewell D.B., Suzuki A.;
RT "Isolation and structure of the Streptococcus faecalis sex pheromone,
RT cAM373.";
RL FEBS Lett. 206:69-72(1986).
CC -!- FUNCTION: cAM373 induces mating response of donor cells harboring
CC -!- MISCELLANEOUS: The N-terminus is possibly responsible for
CC specificity of pheromones to plasmids.
DR PIR; A25269; A25269.
KW Direct protein sequencing; Pheromone.
SQ SEQUENCE 7 AA; 734 MW; 75BDD72059C05DB0 CRC64;
Query Match 28.1%; Score 9; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 FTL 3
Db 3 FIL 5
RESULT 12
P82445 PRELIMINARY; PRT; 7 AA.
ID P82445
AC P82445;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 10 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL.
CC -!- TISSUE SPECIFICITY: XYLEM.
DR GO; GO:0005618; C:cell wall; IEA.
KW Cell wall.

FT NON TER 7 7
SQ SEQUENCE 7 AA; 758 MW; 69D2C1E862D1B2A0 CRC64;
Query Match 28.1%; Score 9; DB 2; Length 7;
Best Local Similarity 33.3%; Pred. No. 1.8e+06;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 LTI 5
Db 1 VTV 3
RESULT 13
O07354 PRELIMINARY; PRT; 7 AA.
ID O07354
AC O07354;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NifK (Fragment).
GN Name=nifK;
OS Synechococcus sp. (strain PCC 8801 / RF-1) (Cyanothecae PCC 8801).
OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
OX NCBI_TaxID=41431;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RF-1;
RX MEDLINE=99231861; PubMed=10217509;
RA Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
RT "Organization and expression of nitrogen-fixation genes in the aerobic
RT nitrogen-fixing unicellular cyanobacterium Synechococcus sp. strain
RT RF-1.";
RL Microbiology 145:743-753(1999).
DR EMBL; AF003700; AAC35193.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 849 MW; 7412C72AA9D5B030 CRC64;
Query Match 28.1%; Score 9; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 FTL 3
Db 3 FDL 5
RESULT 14
Q8JE81 PRELIMINARY; PRT; 7 AA.
ID Q8JE81
AC Q8JE81;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Truncated pol protein (Fragment).
GN Name=pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22056123; PubMed=12060770;
RA Beerenwinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,
RA Hoffmann D., Korn K., Selbig J.;
RT "Diversity and complexity of HIV-1 drug resistance: a bioinformatics
RT approach to predicting phenotype from genotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).
DR EMBL; AF347267; AAK32344.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 885 MW; 76C37731A046C700 CRC64;
Query Match 28.1%; Score 9; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
Db 4 TL 5

RESULT 15
AL14_CARMA
ID AL14_CARMA STANDARD; PRT; 5 AA.
AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Carcinustatin 14.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H.; Johnsen A.H.; Maestro J.-L.; Scott A.G.; Jaros P.P.;
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas."
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -!- SIMILARITY: Belongs to the allatostatin family.
KW Amidation; Direct protein sequencing; Multigene family; Neuropeptide.
FT MOD RES 5 Leucine amide (Potential).
SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 25.0%; Score 8; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3
Db 3 FGL 5

Search completed: November 4, 2004, 01:23:16
Job time : 100.667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:54:10 ; Search time 92.3333 Seconds
(without alignments)
27.196 Million cell updates/sec

Title: US-09-712-819D-1
Perfect score: 32
Sequence: 1 FTLTSS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 116873

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	28	87.5	7	2 AAY40738	Aay40738 S4 deriva
2	28	87.5	7	3 AAB30076	Aab30076 Scaffold
3	25	78.1	7	2 AAY40737	Aay40737 S4 deriva
4	25	78.1	7	3 AAB30075	Aab30075 Scaffold
5	24	75.0	7	2 AAY40736	Aay40736 S4 deriva
6	24	75.0	7	3 AAB30074	Aab30074 Scaffold
7	22	68.8	6	8 ADG63308	Adg63308 Antibody
8	21	65.6	7	2 AAY40735	Aay40735 S4 deriva
9	21	65.6	7	3 AAB30073	Aab30073 Scaffold
10	20	62.5	5	5 AAU85454	Aau85454 Human col
11	20	62.5	6	8 ADP29477	Adp29477 Human sec
12	19	59.4	6	4 AAM51422	Aam51422 Integrin
13	18	56.2	5	6 ABR55418	Abr55418 Amino aci
14	18	56.2	7	2 AAW58711	Aaw58711 Tryptic 4
15	18	56.2	7	3 AAY64225	Aay64225 Cadherin-
16	18	56.2	7	5 ABB84102	Abb84102 Human sin
17	18	56.2	7	8 ADG39396	Adg39396 Tryptic 4
18	18	56.2	7	8 ADO03767	Ado03767 Human CLM
19	17	53.1	5	6 ABU12234	Abu12234 Streptoco
20	17	53.1	5	6 ABU12235	Abu12235 Streptoco
21	17	53.1	6	2 AAW39453	Aaw39453 Human T c
22	17	53.1	6	2 AAW75358	Aaw75358 Hexapepti
23	17	53.1	6	2 AAW75290	Aaw75290 Hexapepti
24	17	53.1	6	6 AAE31832	Aae31832 Androgen
25	17	53.1	6	8 ADL15755	Adl15755 Novel tra

26	17	53.1	7	2 AAR07656	Aar07656 Ribonucle
27	17	53.1	7	2 AAY40723	Aay40723 S3 deriva
28	17	53.1	7	3 AAB30062	Aab30062 Scaffold
29	17	53.1	7	4 AAM44200	Aam44200 H11 bindi
30	17	53.1	7	4 AAM44205	Aam44205 H11 bindi
31	16	50.0	6	1 AAP93345	Aap93345 Portion o
32	16	50.0	6	2 AAR93089	Aar93089 GAL4 DNA
33	16	50.0	6	2 AAW61443	Aaw61443 Gal 4 pro
34	16	50.0	6	2 AAW76753	Aaw76753 Murine si
35	16	50.0	6	2 AAW92487	Aaw92487 Murine Ga
36	16	50.0	6	3 AAY90491	Aay90491 GAL4 DNA
37	16	50.0	6	3 AAB03571	Aab03571 Nuclear c
38	16	50.0	6	4 AAB36961	Aab36961 Peptide #
39	16	50.0	6	4 AAB60836	Aab60836 Peptide #
40	16	50.0	6	5 ABJ11455	Abj11455 Human 125
41	16	50.0	6	5 AAE28111	Aae28111 Human imm
42	16	50.0	6	6 ABU72693	Abu72693 Novel pro
43	16	50.0	6	6 ABR45358	Abr45358 Staphyloc
44	16	50.0	6	6 ABR46478	Abr46478 Staphyloc
45	16	50.0	6	6 ABR44966	Abr44966 Staphyloc

ALIGNMENTS

RESULT 1
AAY40738
ID AAY40738 standard; peptide; 7 AA.
XX
AC AAY40738;
XX
DT 01-DEC-1999 (first entry)
XX
DE S4 derivative #12, beta strand of scaffold protein structure.
XX
KW Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
KW tumour; chemotherapeutic agent.
XX
OS Synthetic.
XX
PN EP947582-A1.
XX
PD 06-OCT-1999.
XX
PF 31-MAR-1998; 98EP-00870065.
XX
PR 31-MAR-1998; 98EP-00870065.
XX
(INNO-) INNOGENETICS NV.
Desmet J, Hufton S, Hoogenboom H, Sablon E;
WPI; 1999-542958/46.
New scaffold protein, useful for stabilizing antigens used as vaccines.
Disclosure; Page 6; 105pp; English.
Sequences AAY40727-Y40748 are functionally equivalent derivatives of the S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-Y40609) together form a single-chain scaffold protein which contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at least 6 beta-strands. The scaffold protein is constructed of beta strands S1-S6, and may also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to the next by hydrogen bonds, which generate a beta sandwich architecture. If the additional beta strands A1-A3 are included in the structure the scaffold is constructed of two beta sheets, with the structures A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each other via amino acid loops, where at least one of the loops binds to a receptor or antigen. The scaffold protein is used to stabilize antigens

CC or whole proteins such as receptors, or their fragments. It may be used
CC to bind two separate molecules. For example, one surface of the scaffold
CC may be bound to a protein which binds to a tumour antigen. This will
CC target the complex to tumour cells. Another surface may be bound to a
CC cytotoxic molecule or an autoimmune antibody which may then kill the
CC tumour cells. Therefore the scaffold protein may be used to target
CC chemotherapeutic agents to specific cells. It may also be used in
CC stabilize individual peptides in a peptide library and may be used in
CC diagnostic techniques, and to stabilize antigens used as vaccines
XX
SQ Sequence 7 AA;

Query Match 87.5%; Score 28; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTIS 6
|
|
|
|
|
|
Db 2 FTLTIS 7

RESULT 2
AAB30076
ID AAB30076 standard; peptide; 7 AA.

XX AAB30076;
XX
DT 09-FEB-2001 (first entry)
XX
DE Scaffold protein SCA S4 peptide SEQ ID NO: 137.

XX Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
KW SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis;
KW diabetic retinopathy; atherosclerosis.

XX Synthetic.

XX WO2000060070-A1.

XX 12-OCT-2000.

XX 01-APR-1999; 99WO-EP002283.

XX 01-APR-1999; 99WO-EP002283.

XX (INNO-) INNOGENETICS NV.

XX Desmet J, Hufton S, Hoogenboom H, Sablon E;

XX WPI; 2000-665002/64.

XX Scaffold composed of single-chain polypeptide having beta sandwich
PT architecture carrying new and randomized peptide sequences useful as
PT supporting framework and carrying antigen- or receptor binding fragments.

XX Disclosure; Page 15; 68pp; English.

XX The present invention is concerned with producing scaffold proteins based
CC upon the human CTLA-4 SCA domain. These scaffold proteins can be used as
CC a scaffold to bind antigen- or receptor-binding fragments. These can be
CC used in the treatment of diseases such as cancer, atherosclerosis,
CC thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy.
CC Sequences AAB29930-B29939 were used in the production of the proteins of
CC the invention

XX Sequence 7 AA;

Query Match 87.5%; Score 28; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTIS 6
|
|
|
|
|
|

Db 2 FTLTIS 7

RESULT 3

AAY40737

ID AAY40737 standard; peptide; 7 AA.

XX AAY40737;

XX 01-DEC-1999 (first entry)

XX S4 derivative #11, beta strand of scaffold protein structure.

XX Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
KW tumour; chemotherapeutic agent.

XX Synthetic.

XX EP947582-A1.

XX 06-OCT-1999.

XX 31-MAR-1998; 98EP-00870065.

XX 31-MAR-1998; 98EP-00870065.

XX (INNO-) INNOGENETICS NV.

XX Desmet J, Hufton S, Hoogenboom H, Sablon E;

XX WPI; 1999-542958/46.

XX New scaffold protein, useful for stabilizing antigens used as vaccines.

XX Disclosure; Page 6; 105pp; English.

XX Sequences AAY40727-Y40748 are functionally equivalent derivatives of the
CC S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a
CC beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-
CC Y40609) together form a single-chain scaffold protein which contains at
CC least 1 disulfide bond, contains less than 10% alpha helix and contains
CC at least 6 beta-strands. The scaffold protein is constructed of beta
CC strands S1-S6, and may also include beta strands A1-A3, or any
CC functionally equivalent derivative of these sequences. The beta strands
CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to
CC the next by hydrogen bonds, which generate a beta sandwich architecture.
CC If the additional beta strands A1-A3 are included in the structure the
CC scaffold is constructed of two beta sheets, with the structures
CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each
CC other via amino acid loops, where at least one of the loops binds to a
CC receptor or antigen. The scaffold protein is used to stabilize antigens
CC or whole proteins such as receptors, or their fragments. It may be used
CC to bind two separate molecules. For example, one surface of the scaffold
CC may be bound to a protein which binds to a tumour antigen. This will
CC target the complex to tumour cells. Another surface may be bound to a
CC cytotoxic molecule or an autoimmune antibody which may then kill the
CC tumour cells. Therefore the scaffold protein may be used to target
CC chemotherapeutic agents to specific cells. It may also be used in
CC stabilize individual peptides in a peptide library and may be used in
CC diagnostic techniques, and to stabilize antigens used as vaccines
XX

SQ Sequence 7 AA;

Query Match 78.1%; Score 25; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTIS 6

Db 2 YTLTIS 7

RESULT 4

AAB30075
ID AAB30075 standard; peptide; 7 AA.
XX
AC AAB30075;
XX
DT 09-FEB-2001 (first entry)
XX
DE Scaffold protein SCA S4 peptide SEQ ID NO: 136.
XX
KW Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
KW SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;
KW diabetic retinopathy; atherosclerosis.
XX
OS Synthetic.
XX
PN WO200060070-A1.
XX
PD 12-OCT-2000.
XX
PF 01-APR-1999; 99WO-EP002283.
XX
PR 01-APR-1999; 99WO-EP002283.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Desmet J, Hufton S, Hoogenboom H, Sablon E;
XX WPI; 2000-665002/64.
DR
PT Scaffold composed of single-chain polypeptide having beta sandwich
PT architecture carrying new and randomized peptide sequences useful as
PT supporting framework and carrying antigen- or receptor binding fragments.
XX
PS Disclosure; Page 15; 68pp; English.
XX
CC The present invention is concerned with producing scaffold proteins based
CC upon the human CTLA-4 SCA domain. These scaffold proteins can be used as
CC a scaffold to bind antigen- or receptor-binding fragments. These can be
CC used in the treatment of diseases such as cancer, atherosclerosis,
CC thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy.
CC Sequences AAB29930-B29939 were used in the production of the proteins of
CC the invention
XX
SQ Sequence 7 AA;
Query Match 78.1%; Score 25; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLTIS 6
Db :|||||
2 YTLTIS 7
RESULT 5
AAY40736
ID AAY40736 standard; peptide; 7 AA.
XX
AC AAY40736;
XX
DT 01-DEC-1999 (first entry)
XX
DE S4 derivative #10, beta strand of scaffold protein structure.
XX
KW Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
KW tumour; chemotherapeutic agent.
XX
OS Synthetic.
XX
PN EP947582-A1.
XX
PD 06-OCT-1999.
XX

PF 31-MAR-1998; 98EP-00870065.
XX
PR 31-MAR-1998; 98EP-00870065.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Desmet J, Hufton S, Hoogenboom H, Sablon E;
XX WPI; 1999-542958/46.
DR
XX New scaffold protein, useful for stabilizing antigens used as vaccines.
XX
PS Disclosure; Page 6; 105pp; English.
XX
CC Sequences AAY40727-Y40748 are functionally equivalent derivatives of the
CC S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a
CC beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-
CC Y40609) together form a single-chain scaffold protein which contains at
CC least 1 disulfide bond, contains less than 10% alpha helix and contains
CC at least 6 beta-strands. The scaffold protein is constructed of beta
CC strands S1-S6, and may also include beta strands A1-A3, or any
CC functionally equivalent derivative of these sequences. The beta strands
CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to
CC the next by hydrogen bonds, which generate a beta sandwich architecture.
CC If the additional beta strands A1-A3 are included in the structure the
CC scaffold is constructed of two beta sheets, with the structures
CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each
CC other via amino acid loops, where at least one of the loops binds to a
CC receptor or antigen. The scaffold protein is used to stabilize antigens
CC or whole proteins such as receptors, or their fragments. It may be used
CC to bind two separate molecules. For example, one surface of the scaffold
CC may be bound to a protein which binds to a tumour antigen. This will
CC target the complex to tumour cells. Another surface may be bound to a
CC cytotoxic molecule or an autoimmune antibody which may then kill the
CC tumour cells. Therefore the scaffold protein may be used to target
CC chemotherapeutic agents to specific cells. It may also be used to
CC stabilize individual peptides in a peptide library and may be used in
CC diagnostic techniques, and to stabilize antigens used as vaccines
XX
SQ Sequence 7 AA;
Query Match 75.0%; Score 24; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLTIS 6
Db :|||||
2 FTLTIS 7
RESULT 6
AAB30074
ID AAB30074 standard; peptide; 7 AA.
XX
AC AAB30074;
XX
DT 09-FEB-2001 (first entry)
XX
DE Scaffold protein SCA S4 peptide SEQ ID NO: 135.
XX
KW Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
KW SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;
KW diabetic retinopathy; atherosclerosis.
XX
OS Synthetic.
XX
PN WO200060070-A1.
XX
PD 12-OCT-2000.
XX
PF 01-APR-1999; 99WO-EP002283.
XX
PR 01-APR-1999; 99WO-EP002283.

XX (INNO-) INNOGENETICS NV.
XX Desmet J, Hufton S, Hoogenboom H, Sablon E;
XX WPI; 2000-665002/64.
XX Scaffold composed of single-chain polypeptide having beta sandwich
PT architecture carrying new and randomized peptide sequences useful as
PT supporting framework and carrying antigen- or receptor binding fragments.
XX
PS Disclosure; Page 15; 68pp; English.
XX The present invention is concerned with producing scaffold proteins based
CC upon the human CTIA-4 SCA domain. These scaffold proteins can be used as
CC a scaffold to bind antigen- or receptor-binding fragments. These can be
CC used in the treatment of diseases such as cancer, atherosclerosis,
CC thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy.
CC Sequences AAB29930-B29939 were used in the production of the proteins of
CC the invention
XX
SQ Sequence 7 AA;
Query Match 75.0%; Score 24; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLTIS 6
Db 2 FTLTIS 7
RESULT 7
ADG63308
ID ADG63308 standard; peptide; 6 AA.
XX
AC ADG63308;
XX
DT 11-MAR-2004 (first entry)
XX
DE Antibody 734 heavy chain variable region last 6 amino acids.
XX
KW cytostatic; virucide; antifungal; antiparasitic; antibacterial;
KW protozoacide; gene therapy; diagnosis; tumor; fungus; parasite;
KW bacterium; protozoan; mycoplasma; acid cation chelator.
XX
OS Homo sapiens.
XX
PN WO2003097105-A1.
XX
PD 27-NOV-2003.
XX
PF 16-MAY-2003; 2003WO-GB002110.
XX
PR 17-MAY-2002; 2002US-00150654.
XX
PA (IMMU-) IMMUNOMEDICS INC.
PA (MCCA/) MCCALL J D.
XX
PI Goldenberg DM, Hansen H, Leung S, McBride WJ, Qu Z;
XX WPI; 2004-042533/04.
XX
PT New compound, useful for preparing a composition for diagnosing or
PT treating tumor or infections caused by fungus, virus, parasite,
PT bacterium, protozoan or mycoplasma.
XX
PS Example 24; SEQ ID NO 18; 119pp; English.
XX
CC The invention relates to a compound, useful for preparing a composition
CC for diagnosing or treating tumor or infections caused by fungus, virus,
CC parasite, bacterium, protozoan or mycoplasma, comprising the formula (I):
CC X-Phe-Lys(HSG)-D-Tyr-Lys(HSG)-Lys(Y)-NH₂ (I). The compound includes a

CC hard acid cation chelator at X or Y, and a soft acid cation chelator at
CC remaining X or Y. The hard acid cation chelator includes a carboxylate or
CC amine group. It comprises NOTA (1,4,7-triazacyclononane-N,N"-triacetic
CC acid), DOFA (1,4,7,10-tetraazacyclododecanetetraacetic acid), DTPA
CC (diethylenetriaminepentaacetic acid), or TETA (p-bromoacetamido-benzyl-
CC tetraethylaminetetraacetic acid). It includes a cation consisting of
CC Group IIA or Group IIIa metal cations. The soft acid cation chelator
CC includes a thiol group. It comprises Tscg-Cys
CC (thiosemicarbazonylglyoxylcysteine) or Tscg-Cys
CC (thiosemicarbazonylacetylcysteine). It includes a cation consisting of
CC transition metals, lanthanides, actinides, Tc, Re or Bi. The compound is
CC useful for preparing a composition for diagnosing or treating tumor or
CC infections caused by fungus, virus, parasite, bacterium, protozoan or
CC mycoplasma. The invention also discloses that the peptide of the
CC invention can be fused or recognised and bound by an antibody, especially
CC a bispecific single chain antibody. This sequence corresponds to the last
CC 6 amino acids of the heavy chain variable region from the human 734
CC antibody. The peptide sequence is used to generate a fusion antibody or
CC fragment that will recognise and bind the peptides of the invention.
XX
SQ Sequence 6 AA;
Query Match 68.8%; Score 22; DB 8; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 TLTISS 7
Db 1 TTVTSS 6
RESULT 8
AAY40735
ID AAY40735 standard; peptide; 7 AA.
XX
AC AAY40735;
XX
DT 01-DEC-1999 (first entry)
XX
DE S4 derivative #9, beta strand of scaffold protein structure.
XX
KW Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
KW tumour; chemotherapeutic agent.
XX
OS Synthetic.
XX
PN EP947582-A1.
XX
PD 06-OCT-1999.
XX
PF 31-MAR-1998; 98EP-00870065.
XX
PR 31-MAR-1998; 98EP-00870065.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Desmet J, Hufton S, Hoogenboom H, Sablon E;
XX WPI; 1999-542958/46.
XX
PT New scaffold protein, useful for stabilizing antigens used as vaccines.
XX
PS Disclosure; Page 6; 105pp; English.
XX
CC Sequences AAY40727-Y40748 are functionally equivalent derivatives of the
CC S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a
CC beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-
CC Y40609) together form a single-chain scaffold protein which contains at
CC least 1 disulfide bond, contains less than 10% alpha helix and contains
CC at least 6 beta-strands. The scaffold protein is constructed of beta
CC strands S1-S6, and may also include beta strands A1-A3, or any
CC functionally equivalent derivative of these sequences. The beta strands
CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to

CC the next by hydrogen bonds, which generate a beta sandwich architecture.
CC If the additional beta strands A1-A3 are included in the structure the
CC scaffold is constructed of two beta sheets, with the structures
CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each
CC other via amino acid loops, where at least one of the loops binds to a
CC receptor or antigen. The scaffold protein is used to stabilize antigens
CC or whole proteins such as receptors, or their fragments. It may be used
CC to bind two separate molecules. For example, one surface of the scaffold
CC may be bound to a protein which binds to a tumour antigen. This will
CC target the complex to tumour cells. Another surface may be bound to a
CC cytotoxic molecule or an autoimmune antibody which may then kill the
CC tumour cells. Therefore the scaffold protein may be used to target
CC chemotherapeutic agents to specific cells. It may also be used to
CC stabilize individual peptides in a peptide library and may be used in
CC diagnostic techniques, and to stabilize antigens used as vaccines
XX
SQ Sequence 7 AA;

Query Match 65.6%; Score 21; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTIS 6
Db :|||||
2 YSLTIS 7

RESULT 9
AAB30073
ID AAB30073 standard; peptide; 7 AA.
XX
AC AAB30073;

XX 09-FEB-2001 (first entry)

DE Scaffold protein SCA S4 peptide SEQ ID NO: 134.

XX Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
KW SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis;
KW diabetic retinopathy; atherosclerosis.

XX Synthetic.

XX WO200060070-A1.

XX 12-OCT-2000.

XX 01-APR-1999; 99WO-EP002283.

XX 01-APR-1999; 99WO-EP002283.

XX (INNO-) INNOGENETICS NV.

XX Desmet J, Hufton S, Hoogenboom H, Sablon E;

XX WPI; 2000-665002/64.

XX Scaffold composed of single-chain polypeptide having beta sandwich
PT architecture carrying new and randomized peptide sequences useful as
PT supporting framework and carrying antigen- or receptor binding fragments.

PS Disclosure; Page 15; 68pp; English.

XX The present invention is concerned with producing scaffold proteins based
CC upon the human CTLA-4 SCA domain. These scaffold proteins can be used as
CC a scaffold to bind antigen- or receptor-binding fragments. These can be
CC used in the treatment of diseases such as cancer, atherosclerosis,
CC thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy.
CC Sequences AAB29930-B29939 were used in the production of the proteins of
CC the invention

XX Sequence 7 AA;

Query Match 65.6%; Score 21; DB 3; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTIS 6
Db :|||||
2 YSLTIS 7

RESULT 10
AAU85454
ID AAU85454 standard; peptide; 5 AA.
XX
AC AAU85454;

XX 21-MAY-2002 (first entry)

XX Human colon specific polypeptide antibody binding site #31.
DE
XX Human; colon specific gene; CSG; cytostatic; metastasis;
KW colon cancer staging; antibody binding site.

XX Homo sapiens.

XX WO200206515-A2.

XX 24-JAN-2002.

XX 17-JUL-2001; 2001WO-US022454.

XX 17-JUL-2000; 2000US-00618596.

XX (DIAD-) DIADEXUS INC.

XX Macina RA, Sun Y;

XX WPI; 2002-171815/22.

XX Diagnosing, staging or monitoring colon cancer involves determining a
PT colon specific gene in cells, tissues or body fluids in patient, and
PT comparing it with levels of the gene from a normal human control.

PS Disclosure; Page 21; 52pp; English.

XX The invention relates to diagnosing the presence of colon cancer,
CC metastases of colon cancer, staging colon cancer, monitoring colon cancer
CC for the onset of metastasis or monitoring a change in stage of colon
CC cancer in a patient. The method involves determining a colon specific
CC gene (CSG) in cells, tissues or bodily fluids and comparing it with
CC levels of CSG in cells, tissues or bodily fluids from a normal human
CC control. Colon cancer can be treated by administering a molecule which
CC down regulates the expression or activity of CSG. An immune response
CC against a target cell expressing CSG can be induced by delivering an
CC immunologically stimulatory amount of a CSG protein to a patient, so that
CC an immune response is mounted. Therapeutic agents are useful for imaging
CC colon cancer in a patient by administering an agent labelled with
CC paramagnetic ions or a radioisotope to the patient. They are also useful
CC for preventing the onset of colon cancer, and in diagnosis and treatment
CC of the disease. Sequences AAU85424-AAU85502 represent human colon
CC specific protein antibody binding sites used in the method of the
CC invention

XX Sequence 5 AA;

Query Match 62.5%; Score 20; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLT 4
Db :|||||
2 FTLT 5

Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTLTISS 7
||: ||
Db 1 FTIDSSS 7

Search completed: November 4, 2004, 01:18:12
Job time : 95.3333 secs

RESULT 15
AAy64225
ID AAY64225 standard; peptide; 7 AA.
XX
AC AAY64225;
XX
DT 02-MAR-2000 (first entry)
XX
DE Cadherin-related neuronal receptor CAR sequence SEQ ID NO:637.
XX
KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
inhibition; cadherin extracellular domain; cell adhesion recognition;
KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
KW neurological disease.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9957149-A2.
XX
PD 11-NOV-1999.
XX
PF 05-MAY-1999; 99WO-CA000363.
XX
PR 05-MAY-1998; 98US-00073040.
PR 06-NOV-1998; 98US-00187859.
PR 20-JAN-1999; 99US-00234395.
PR 08-MAR-1999; 99US-00264516.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuk OW, Gour BJ, Byers S;
XX
DR WPI; 2000-038791/03.
XX
PT New cadherin modulating agents, used for modulating nonclassical cadherin
mediated functions for treating e.g. cancers, obesity, rheumatoid
PT arthritis, multiple sclerosis, diabetes or a neurological disease.
XX
PS Claim 99; Page 216; 252pp; English.
XX
CC The present invention describes cadherin modulating agents (MA)
comprising peptides which comprise a nonclassical cadherin cell adhesion
CC recognition (CAR) sequence. The MAs can be used for modulating
CC nonclassical cadherin-mediated functions. They can be used for e.g.
CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
CC mammal, enhancing delivery of a drug through the skin of a mammal,
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC expressing cell, preventing or treating obesity in a mammal, stimulating
CC blood vessel regression in a mammal, enhancing drug delivery to the
CC central nervous system, treating a demyelinating neurological disease,
CC increasing vasopermeability in a mammal, enhancing adhesion of
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC a mammal, or preventing pregnancy in a mammal. They can also be used for
CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
CC -related macular degeneration, multiple sclerosis and diabetes. The
CC products can also be used for detection and diagnosis and in bioreactors.
CC AAY60592 to AAY64572 represent specifically claimed peptides, and
CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 7 AA;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:42:19 ; Search time 16.6667 Seconds
(without alignments)
27.854 Million cell updates/sec

Title: US-09-712-819D-1
Perfect score: 32
Sequence: 1 FTLTISS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	25	5	PCT-US91-02942-26
2	32	100.0	25	5	PCT-US91-02942-42
3	32	100.0	32	2	US-08-470-139-13
4	32	100.0	32	3	US-08-569-147-40
5	32	100.0	32	3	US-09-347-061-13
6	32	100.0	32	3	US-09-425-638A-92
7	32	100.0	32	3	US-09-425-638A-94
8	32	100.0	32	3	US-09-543-004-92
9	32	100.0	32	3	US-09-543-004-94
10	32	100.0	32	4	US-09-647-468-129
11	32	100.0	32	4	US-09-563-222C-76
12	32	100.0	32	4	US-09-563-222C-86
13	32	100.0	32	4	US-09-563-222C-110
14	32	100.0	32	4	US-09-855-271-13
15	32	100.0	50	5	PCT-US91-02942-8
16	32	100.0	50	5	PCT-US91-02942-9
17	32	100.0	64	2	US-08-765-179B-10
18	32	100.0	64	2	US-08-765-179B-14
19	32	100.0	70	3	US-08-554-840-9
20	32	100.0	70	4	US-08-925-339-9
21	32	100.0	70	4	US-09-332-595-9
22	32	100.0	76	3	US-08-851-362D-21
23	32	100.0	80	3	US-08-554-840-10
24	32	100.0	80	3	US-08-554-840-12
25	32	100.0	80	3	US-08-554-840-13
26	32	100.0	80	3	US-08-554-840-15
27	32	100.0	80	4	US-08-925-339-10

28	32	100.0	80	4	US-08-925-339-12	Sequence 12, Appl
29	32	100.0	80	4	US-08-925-339-13	Sequence 13, Appl
30	32	100.0	80	4	US-08-925-339-15	Sequence 15, Appl
31	32	100.0	80	4	US-09-332-595-10	Sequence 10, Appl
32	32	100.0	80	4	US-09-332-595-12	Sequence 12, Appl
33	32	100.0	80	4	US-09-332-595-13	Sequence 13, Appl
34	32	100.0	80	4	US-09-332-595-15	Sequence 15, Appl
35	32	100.0	80	4	US-09-269-921-130	Sequence 130, Appl
36	32	100.0	93	3	US-08-783-853A-35	Sequence 35, Appl
37	32	100.0	93	3	US-09-344-050-35	Sequence 35, Appl
38	32	100.0	95	2	US-08-290-592E-19	Sequence 19, Appl
39	32	100.0	95	2	US-08-290-592E-33	Sequence 33, Appl
40	32	100.0	95	4	US-09-472-087-94	Sequence 94, Appl
41	32	100.0	95	5	PCT-US95-10053-16	Sequence 16, Appl
42	32	100.0	95	5	PCT-US95-10053-30	Sequence 30, Appl
43	32	100.0	95	5	PCT-US96-09448-19	Sequence 19, Appl
44	32	100.0	95	5	PCT-US96-09448-33	Sequence 33, Appl
45	32	100.0	96	3	US-08-466-368-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
PCT-US91-02942-26
; Sequence 26, Application PC/TUS9102942
; GENERAL INFORMATION:
; APPLICANT: ROTHLEIN, ROBERT
; APPLICANT: ADAIR, JOHN R
; APPLICANT: ATHWAL, DILJEET S
; TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Ave. NW Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02942
; FILING DATE: 19910429
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9009549.8
; FILING DATE: 27-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: FOX, SAM L
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 1011.0586600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-02942-26

Query Match 100.0%; Score 32; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FTLTISS 7
Db 8 FTLTISS 14


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RESULT 2
PCT-US91-02942-42
; Sequence 42, Application PC/TUS9102942
; GENERAL INFORMATION:
; APPLICANT: ROTHLEIN, ROBERT
; APPLICANT: ADAIR, JOHN R
; APPLICANT: ATHAL, DIJJEET S
; TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Ave. NW Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02942
; FILING DATE: 19910429
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9009549.8
; FILING DATE: 27-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: FOX, SAM L
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 1011.0586600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-02942-42

Query Match 100.0%; Score 32; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 8 FTLTISS 14

RESULT 3
US-08-470-139-13
; Sequence 13, Application US/08470139
; Patent No. 5998586
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Interleukin-5 specific recombinant antibodies
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,139
; FILING DATE: 06 JUNE-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: TRUJILLO, DOREEN YATKO
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; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0044
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-470-139-13

Query Match 100.0%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 15 FTLTISS 21

RESULT 4
US-08-569-147-40
; Sequence 40, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANISED ANTIBODIES
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 6180377ris, LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,147
; FILING DATE: 25-March-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yatko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-569-147-40

Query Match 100.0%; Score 32; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 15 FTLTISS 21

RESULT 5
US-09-347-061-13
; Sequence 13, Application US/09347061
```



```
; Patent No. 6316227
; GENERAL INFORMATION:
; APPLICANT: Bodmer, Mark
; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Entage, John Spencer
; TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
; FILE REFERENCE: CARP-0071
; CURRENT APPLICATION NUMBER: US/09/347,061
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Consensus
US-09-347-061-13

Query Match          100.0%; Score 32; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
   |||||
Db 15 FTLTISS 21

RESULT 6
US-09-425-638A-92
; Sequence 92, Application US/09425638A
; Patent No. 6342587
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO
; FILE REFERENCE: LUD 5630
; CURRENT APPLICATION NUMBER: US/09/425,638A
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 92
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-425-638A-92

Query Match          100.0%; Score 32; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
   |||||
Db 15 FTLTISS 21

RESULT 7
US-09-425-638A-94
; Sequence 94, Application US/09425638A
; Patent No. 6342587
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO
; FILE REFERENCE: LUD 5630
; CURRENT APPLICATION NUMBER: US/09/425,638A
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 94
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
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; FEATURE:
US-09-425-638A-94

Query Match          100.0%; Score 32; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
   |||||
Db 15 FTLTISS 21

RESULT 8
US-09-543-004-92
; Sequence 92, Application US/09543004
; Patent No. 6346249
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO
; FILE REFERENCE: LUD 5630.1
; CURRENT APPLICATION NUMBER: US/09/543,004
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/425,638
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 92
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-92

Query Match          100.0%; Score 32; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
   |||||
Db 15 FTLTISS 21

RESULT 9
US-09-543-004-94
; Sequence 94, Application US/09543004
; Patent No. 6346249
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO
; FILE REFERENCE: LUD 5630.1
; CURRENT APPLICATION NUMBER: US/09/543,004
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/425,638
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 94
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-94

Query Match          100.0%; Score 32; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
   |||||
Db 15 FTLTISS 21

RESULT 10
US-09-543-004-94

Query Match          100.0%; Score 32; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
   |||||
Db 15 FTLTISS 21
```

US-09-647-468-129
; Sequence 129, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:

; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 129
; LENGTH: 32
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence
; OTHER INFORMATION: of FR3 of versions "a" of humanized L chain V
; OTHER INFORMATION: region
US-09-647-468-129

Query Match 100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTISS 7
Db 15 FTLTISS 21

RESULT 11

US-09-563-222C-76
; Sequence 76, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:

; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-563-222C-76

Query Match 100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTISS 7
Db 15 FTLTISS 21

RESULT 12

US-09-563-222C-86
; Sequence 86, Application US/09563222C

; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-563-222C-86

Query Match 100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTISS 7
Db 15 FTLTISS 21

RESULT 13

US-09-563-222C-110
; Sequence 110, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222C-110

Query Match 100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTISS 7
Db 15 FTLTISS 21

RESULT 14

US-09-855-271-13
; Sequence 13, Application US/09855271
; Patent No. 6734286
; GENERAL INFORMATION:
; APPLICANT: Bodmer, Mark W
; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Emtage, John Spencer
; TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
; FILE REFERENCE: CARP-0088

Search completed: November 4, 2004, 00:54:51
Job time : 17.6667 secs

; CURRENT APPLICATION NUMBER: US/09/855,271
 ; CURRENT FILING DATE: 2001-05-15
 ; PRIOR APPLICATION NUMBER: 09/347,061
 ; PRIOR FILING DATE: 1999-07-02
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 13
 ; LENGTH: 32
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Consensus
 US-09-855-271-13

Query Match 100.0%; Score 32; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
 Db 15 FTLTISS 21

RESULT 15
 PCT-US91-02942-8
 ; Sequence 8, Application PC/TUS9102942
 ; GENERAL INFORMATION:
 ; APPLICANT: ROTHLEIN, ROBERT
 ; APPLICANT: ADAIR, JOHN R
 ; APPLICANT: ATHWAL, DILJEET S
 ; TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
 ; NUMBER OF SEQUENCES: 102
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 ; STREET: 1225 Connecticut Ave. NW Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US91/02942
 ; FILING DATE: 19910429
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9009549.8
 ; FILING DATE: 27-APR-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: FOX, SAM L
 ; REGISTRATION NUMBER: 30,353
 ; REFERENCE/DOCKET NUMBER: 1011.0586600
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 466-0800
 ; TELEFAX: (202) 833-8716
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 50 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 PCT-US91-02942-8

Query Match 100.0%; Score 32; DB 5; Length 50;
 Best Local Similarity 100.0%; Pred. No. 7.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
 Db 26 FTLTISS 32

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:36:19 ; Search time 19 Seconds
(without alignments)
35.448 Million cell updates/sec

Title: US-09-712-819D-1
Perfect score: 32
Sequence: 1 FTLTISS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	54	2 JT0521	Ig kappa chain V-I
2	32	100.0	71	2 S21526	Ig kappa chain V r
3	32	100.0	77	2 S70443	Ig kappa chain V r
4	32	100.0	77	2 D30502	Ig kappa chain V r
5	32	100.0	78	2 S34102	Ig kappa chain V r
6	32	100.0	79	2 S24215	Ig kappa chain - m
7	32	100.0	81	2 PH1048	Ig light chain V r
8	32	100.0	83	2 S78489	Ig kappa chain V r
9	32	100.0	84	2 S34099	Ig kappa chain V r
10	32	100.0	86	2 S16834	Ig kappa chain V r
11	32	100.0	86	2 S16824	Ig kappa chain V r
12	32	100.0	86	2 S16836	Ig kappa chain V r
13	32	100.0	86	2 S16837	Ig kappa chain V r
14	32	100.0	86	2 S16830	Ig kappa chain V r
15	32	100.0	86	2 S16833	Ig kappa chain V-I
16	32	100.0	86	2 S16829	Ig kappa chain V r
17	32	100.0	86	2 S16826	Ig kappa chain V r
18	32	100.0	86	2 S34086	Ig kappa chain V r
19	32	100.0	86	2 S16840	Ig kappa chain V r
20	32	100.0	87	2 S34084	Ig kappa chain V r
21	32	100.0	87	2 S21523	Ig kappa chain V r
22	32	100.0	87	2 S34097	Ig kappa chain V r
23	32	100.0	87	2 S34083	Ig kappa chain V r
24	32	100.0	87	2 S34098	Ig kappa chain V r
25	32	100.0	88	2 S21525	Ig kappa chain V r
26	32	100.0	88	2 S21522	Ig kappa chain V r
27	32	100.0	88	2 S21528	Ig kappa chain V r
28	32	100.0	88	2 S21520	Ig kappa chain V r
29	32	100.0	88	2 S34104	Ig kappa chain V r

30	32	100.0	91	2 S37521	Ig kappa chain V r
31	32	100.0	91	2 S37511	Ig kappa chain V r
32	32	100.0	91	2 S37525	Ig kappa chain V r
33	32	100.0	91	2 S37515	Ig kappa chain V r
34	32	100.0	91	2 S37527	Ig kappa chain V r
35	32	100.0	91	2 PH1071	Ig light chain V r
36	32	100.0	92	2 S37504	Ig kappa chain V r
37	32	100.0	92	2 S37509	Ig kappa chain V r
38	32	100.0	92	2 S37506	Ig kappa chain V r
39	32	100.0	92	2 S37512	Ig kappa chain V r
40	32	100.0	92	2 S37522	Ig kappa chain V r
41	32	100.0	92	2 S37532	Ig kappa chain V r
42	32	100.0	92	2 S37533	Ig kappa chain V r
43	32	100.0	92	2 S37530	Ig kappa chain V r
44	32	100.0	92	2 S37523	Ig kappa chain V r
45	32	100.0	92	2 S37535	Ig kappa chain V r

ALIGNMENTS

RESULT 1
JT0521
Ig kappa chain V-III region (CP1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Oct-1992 #sequence_revision 23-Oct-1992 #text_change 09-May-1997
C;Accession: JT0521
R;Anker, R.; Conley, M.E.; Pollok, B.A.
J. Exp. Med. 169, 2109-2119, 1989
A;Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglobulinemia
A;Reference number: JT0511; MUID:89279157; PMID:2786547
A;Accession: JT0521
A;Molecule type: mRNA
A;Residues: 1-54 <ANK>
A;Note: the sequence shown here is one of eight productive V-D-J mu chain rearrangements
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-49/Domain: V region <VRE>
F;50-54/Domain: J region <JRE>

Query Match 100.0%; Score 32; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 23 FTLTISS 29

RESULT 2
S21526
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 23-Jul-1999
C;Accession: S34082; S21526
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed in a clonal fashion
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34082
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-71 <WA2>
A;Cross-references: EMBL:X66042; NID:G33318; PIDN:CAA46841.1; PID:G33319
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
|||||

Db 64 FTLTISS 70

RESULT 3

S70443

Ig kappa chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 07-May-1999

C;Accession: S70443

R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.

Mol. Immunol. 29, 1363-1373, 1992

A;Title: Igm kappa/lambda EBV human B cell clone: an early step of differentiation of fe

A;Reference number: S70442; MUID:93024508; PMID:1383695

A;Accession: S70443

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-77 <CUI>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 100.0%; Score 32; DB 2; Length 77;

Best Local Similarity 100.0%; Pred. No. 2.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7

Db 40 FTLTISS 46

RESULT 4

D30502

Ig kappa chain V region (D44) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 03-Nov-1988 #sequence_revision 03-Aug-1992 #text_change 23-Jul-1999

C;Accession: D30502

R;Ellat, D.; Webster, D.M.; Rees, A.R.

J. Immunol. 141, 1745-1753, 1988

A;Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mic

A;Reference number: A30502; MUID:88315787; PMID:2457627

A;Accession: D30502

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-77 <EIL>

A;Cross-references: GB:M21908; NID:g197073; PIDN:AAA38908.1; PID:g197074

A;Note: the authors translated the codon CAG for residue 48 as Pro

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 77;

Best Local Similarity 100.0%; Pred. No. 2.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7

Db 40 FTLTISS 46

RESULT 5

S34102

Ig kappa chain V region - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-May-1999

C;Accession: S34102

R;Wagner, S.D.; Luzzatto, L.

Eur. J. Immunol. 23, 391-397, 1993

A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute

A;Reference number: S34076; MUID:93170387; PMID:8436174

A;Accession: S34102

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-78 <WAG>

A;Cross-references: EMBL:X67186

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 78;

Best Local Similarity 100.0%; Pred. No. 2.8;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7

Db 62 FTLTISS 68

RESULT 6

S24215

Ig kappa chain - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S24215

R;Shimizu, T.; Iwasato, T.; Yamagishi, H.

J. Exp. Med. 173, 1065-1072, 1991

A;Title: Deletions of immunoglobulin C(kappa) region characterized by the circular exci

A;Reference number: S24214; MUID:91217618; PMID:1902500

A;Accession: S24215

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-79 <SHI>

A;Cross-references: EMBL:X58202; NID:g53718; PIDN:CAA41178.1; PID:g930195

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 79;

Best Local Similarity 100.0%; Pred. No. 2.8;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7

Db 44 FTLTISS 50

RESULT 7

PH1048

Ig light chain V region (clone 165.49) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996

C;Accession: PH1048

R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective B

A;Reference number: PH0971; MUID:92381444; PMID:1512540

A;Accession: PH1048

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-81 <TIL>

A;Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 81;

Best Local Similarity 100.0%; Pred. No. 2.9;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7

Db 56 FTLTISS 62

RESULT 8

S78489

Ig kappa chain V region (patient 28) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Apr-1998 #sequence_revision 08-May-1998 #text_change 21-Jan-2000

C;Accession: S78489; S34100

R;Wagner, S.

submitted to the EMBL Data Library, July 1992

A;Reference number: S78488

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A;Accession: S78489
A;Molecule type: DNA
A;Residues: 1-83 <WAG>
A;Cross-references: EMBL:X67184
A;Experimental source: patient 28
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34100
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-68,'Q','70-73','A','75-83 <WAW>
A;Cross-references: EMBL:X67184
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;6-80/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 32; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
    |||||
Db 61 FTLTISS 67

RESULT 9
S34099
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S34099
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34099
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-84 <WAG>
A;Cross-references: UNIPROT:Q9UL83; EMBL:X67183
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;5-79/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 32; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
    |||||
Db 60 FTLTISS 66

RESULT 10
S16834
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16834
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16834
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-86 <BLA>
A;Cross-references: EMBL:X54832
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>

A;Accession: S78489
A;Molecule type: DNA
A;Residues: 1-83 <WAG>
A;Cross-references: EMBL:X67184
A;Experimental source: patient 28
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34100
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-68,'Q','70-73','A','75-83 <WAW>
A;Cross-references: EMBL:X67184
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;6-80/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 32; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
    |||||
Db 61 FTLTISS 67

RESULT 9
S34099
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S34099
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34099
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-84 <WAG>
A;Cross-references: UNIPROT:Q9UL83; EMBL:X67183
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;5-79/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 32; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
    |||||
Db 60 FTLTISS 66

RESULT 10
S16834
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16834
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16834
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-86 <BLA>
A;Cross-references: EMBL:X54832
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>
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Query Match      100.0%; Score 32; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
    |||||
Db 62 FTLTISS 68

RESULT 11
S16824
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16824
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fa
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16824
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-86 <BLA>
A;Cross-references: EMBL:X54822
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 32; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
    |||||
Db 62 FTLTISS 68
```

```
RESULT 12
S16836
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16836
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16836
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-86 <BLA>
A;Cross-references: EMBL:X54834
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>
```

```
Query Match      100.0%; Score 32; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
    |||||
Db 62 FTLTISS 68
```

```
RESULT 13
S16837
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16837
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
```

Eur. J. Immunol. 21, 1221-1227, 1991	
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac	
A;Reference number: S16823; MUID:91243737; PMID:1903706	
A;Accession: S16837	
A;Status: preliminary; translation not shown	
A;Molecule type: mRNA	
A;Residues: 1-86 <BLA>	
A;Cross-references: EMBL:X54835	
C;Superfamily: immunoglobulin V region; immunoglobulin homology	
C;Keywords: heterotetramer; immunoglobulin	
F;7-81/Domain: immunoglobulin homology <IMM>	
Query Match 100.0%; Score 32; DB 2; Length 86;	
Best Local Similarity 100.0%; Pred. No. 3.1;	
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 FTLTISS 7	
Db 62 FTLTISS 68	
RESULT 14	
S16830	
Ig kappa chain V region - human (fragment)	
C;Species: Homo sapiens (man)	
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000	
C;Accession: S16830	
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.	
Eur. J. Immunol. 21, 1221-1227, 1991	
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac	
A;Reference number: S16823; MUID:91243737; PMID:1903706	
A;Accession: S16830	
A;Status: preliminary; translation not shown	
A;Molecule type: mRNA	
A;Residues: 1-86 <BLA>	
A;Cross-references: EMBL:X54828	
C;Superfamily: immunoglobulin V region; immunoglobulin homology	
C;Keywords: heterotetramer; immunoglobulin	
F;7-81/Domain: immunoglobulin homology <IMM>	
Query Match 100.0%; Score 32; DB 2; Length 86;	
Best Local Similarity 100.0%; Pred. No. 3.1;	
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 FTLTISS 7	
Db 62 FTLTISS 68	
RESULT 15	
S16833	
Ig kappa chain V-III region - human (fragment)	
C;Species: Homo sapiens (man)	
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000	
C;Accession: S16833; S16838	
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.	
Eur. J. Immunol. 21, 1221-1227, 1991	
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac	
A;Reference number: S16823; MUID:91243737; PMID:1903706	
A;Accession: S16833	
A;Status: translation not shown	
A;Molecule type: mRNA	
A;Residues: 1-86 <BLA>	
A;Cross-references: EMBL:X54831	
A;Experimental source: clone bkv17	
A;Accession: S16838	
A;Status: translation not shown	
A;Molecule type: mRNA	
A;Residues: 1-86 <BLW>	
A;Cross-references: EMBL:X54836	
A;Experimental source: clone slkv14	
C;Superfamily: immunoglobulin V region; immunoglobulin homology	
C;Keywords: heterotetramer; immunoglobulin	

F;7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7

Db 62 FTLTISS 68

Search completed: November 4, 2004, 00:48:40
Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:41:09 ; Search time 103 Seconds
(without alignments)
39.103 Million cell updates/sec

Title: US-09-712-819D-1

Perfect score: 32

Sequence: 1 FTLTISS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	32	100.0	78	2 Q7VR58	Q7vr58 candidatus
2	32	100.0	81	2 AAR10995	Aar10995 mus muscu
3	32	100.0	93	2 AAR11030	Aar11030 mus muscu
4	32	100.0	101	2 AAR11008	Aar11008 mus muscu
5	32	100.0	107	1 KVID_HUMAN	P01596 homo sapien
6	32	100.0	107	2 Q96SA9	Q96sa9 homo sapien
7	32	100.0	107	2 Q9ERZ9	Q9erz9 mus musculu
8	32	100.0	108	1 KVI1F_HUMAN	P01598 homo sapien
9	32	100.0	108	1 KVI1G_HUMAN	P01599 homo sapien
10	32	100.0	108	1 KVI1H_HUMAN	P01600 homo sapien
11	32	100.0	108	1 KVI1S_HUMAN	P01611 homo sapien
12	32	100.0	108	1 KV5Q_MOUSE	P01650 mus musculu
13	32	100.0	108	1 KV5R_MOUSE	P01651 mus musculu
14	32	100.0	108	1 KV5S_MOUSE	P01652 mus musculu
15	32	100.0	108	1 KV5T_MOUSE	P01653 mus musculu
16	32	100.0	108	2 Q9UL70	Q9ul70 homo sapien
17	32	100.0	108	2 Q9UL77	Q9ul77 homo sapien
18	32	100.0	108	2 Q9UL83	Q9ul83 homo sapien
19	32	100.0	109	1 KVI1T_HUMAN	P01612 homo sapien
20	32	100.0	109	1 KV3F_HUMAN	P01624 homo sapien
21	32	100.0	109	2 Q9UL85	Q9ul85 homo sapien
22	32	100.0	114	1 KVI1A_MOUSE	P01632 mus musculu
23	32	100.0	114	1 KV4A_HUMAN	P01625 homo sapien
24	32	100.0	115	1 KV3I_HUMAN	P04433 homo sapien
25	32	100.0	116	1 KV3J_HUMAN	P04434 homo sapien
26	32	100.0	116	2 AAR11065	Aar11065 mus muscu
27	32	100.0	117	1 KVI1I_HUMAN	P01601 homo sapien
28	32	100.0	117	1 KVI1J_HUMAN	P01602 homo sapien
29	32	100.0	118	2 AAR11001	Aar11001 mus muscu
30	32	100.0	121	1 KV40_HUMAN	P06312 homo sapien
31	32	100.0	129	1 KVI1W_HUMAN	P04431 homo sapien

32	32	100.0	129	1 KV1X_HUMAN	P04432 homo sapien
33	32	100.0	133	1 KV4B_HUMAN	P06313 homo sapien
34	32	100.0	134	1 KV4C_HUMAN	P06314 homo sapien
35	32	100.0	136	1 KV5B_MOUSE	P01634 mus musculu
36	32	100.0	174	2 BAC03964	Bac03964 homo sapi
37	32	100.0	234	2 AAH30813	Aah30813 homo sapi
38	32	100.0	236	2 Q6PIH7	Q6pih7 homo sapien
39	32	100.0	236	2 Q6PIT5	Q6pit5 homo sapien
40	32	100.0	236	2 Q6GMW1	Q6gmw1 homo sapien
41	32	100.0	236	2 Q6GMX0	Q6gmw0 homo sapien
42	32	100.0	236	2 Q6GMX8	Q6gmw8 homo sapien
43	32	100.0	236	2 Q6GMX9	Q6gmw9 homo sapien
44	32	100.0	236	2 Q7Z3Y4	Q7z3y4 homo sapien
45	32	100.0	236	2 AAH29444	Aah29444 homo sapi

ALIGNMENTS

RESULT 1

Q7VR58
ID Q7VR58 PRELIMINARY; PRT; 78 AA.
AC Q7VR58;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Major outer membrane lipoprotein.
GN Name=lpp; OrderedLocusNames=Bfl364;
OS Candidatus Blochmannia floridanus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.
OX NCBI_TaxID=203907;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22784745; PubMed=12886019;
RA Gil R., Silva F.J., Zientz E., Delmotte F., Gonzalez-Candela F.,
Latorre A., Rausell C., Kamerbeek J., Gadau J., Hoeldobler B.,
van Ham R.C.H.J., Gross R., Moya A.;
RT "The genome sequence of Blochmannia floridanus: comparative analysis of reduced genomes.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:9388-9393(2003).
DR EMBL; BX248585; CAD83431.1; -.
KW Complete proteome; Lipoprotein.
SQ SEQUENCE 78 AA; 8906 MW; 4AA330089FOA0EC2 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 9 FTLTISS 15

RESULT 2

AAR10995
ID AAR10995 PRELIMINARY; PRT; 81 AA.
AC AAR10995;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.Sle1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.Sle1 mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
EMBL; AY436835; AAR10995.1; -.

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FT NON_TER 1 1
FT NON_TER 81 81
SQ SEQUENCE 81 AA; 8929 MW; D2326578184F801C CRC64;

Query Match
Best Local Similarity 100.0%; Score 32; DB 2; Length 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 50 FTLTISS 56

RESULT 3
AAR11030
ID AAR11030 PRELIMINARY; PRT; 93 AA.
AC AAR11030;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.Sle1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.Sle1 mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436870; AAR11030.1; -.
FT NON_TER 1 1
FT NON_TER 93 93
SQ SEQUENCE 93 AA; 10180 MW; CAE53E27EABC45E7 CRC64;

Query Match
Best Local Similarity 100.0%; Score 32; DB 2; Length 93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 67 FTLTISS 73

RESULT 4
AAR11008
ID AAR11008 PRELIMINARY; PRT; 101 AA.
AC AAR11008;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.Sle1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.Sle1 mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436848; AAR11008.1; -.
FT NON_TER 1 1
FT NON_TER 101 101
SQ SEQUENCE 101 AA; 11166 MW; 593AC4478AD607BB CRC64;

Query Match
Best Local Similarity 100.0%; Score 32; DB 2; Length 101;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
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```
Db 75 FTLTISS 81

RESULT 5
KV1D_HUMAN
ID KV1D_HUMAN STANDARD; PRT; 107 AA.
AC P01596;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region CAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75075135; PubMed=4216454;
RA Milstein C.P., Deverson E.V.;
RT "Primary structure of kappa light chain from a human myeloma protein.";
RL Eur. J. Biochem. 49:377-391(1974).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (1,2) marker.
CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein.
DR PIR; A01864; KIHUAR.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Glycoprotein; Immunoglobulin V region.
FT CARBOHYD 28 28 N-linked (GlcNAc...).
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11703 MW; E1BF0DF9844C3346 CRC64;

Query Match
Best Local Similarity 100.0%; Score 32; DB 1; Length 107;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 71 FTLTISS 77

RESULT 6
Q96SA9
ID Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
DR PIR; B49047; B49047.
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DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSSP; P01607; 1BWV.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match      100.0%; Score 32; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 71 FTLTISS 77

RESULT 7
Q9ERZ9 PRELIMINARY; PRT; 107 AA.
AC Q9ERZ9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti human TNF-alpha light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT "Construction and sequencing of the single-chain antibody gene of a
RT human TNF-alpha specific monoclonal antibody.";
RL Di 4 Jun Yi Da Xue Xue Bao 19:373-376(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
RT "Cloning and sequencing of the light chain fragment of variable region
RT genes of an anti-hTNF-a monoclonal antibody.";
RL Xibao Yu Fenzi Mianyixue Zazhi 12:21-26(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF262753; AAG33804.1; -.
DR PDB; 2AP2; X-ray; A/C=1-107.
DR PDB; 43C9; X-ray; A/C/E/G=1-107.
DR PDB; 43CA; X-ray; A/C/E/G=1-107.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 107
SQ SEQUENCE 107 AA; 11784 MW; 2B15EEA6604A26C3 CRC64;

Query Match      100.0%; Score 32; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 74 FTLTISS 80
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```
RESULT 8
KV1F_HUMAN
ID KV1F_HUMAN STANDARD; PRT; 108 AA.
AC P01598;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71064023; PubMed=5489770;
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT acid sequence of the light chain.";
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein.
DR PIR; A90562; K1HUEU.
DR HSSP; P01607; 1BWV.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Complementarity-determining-3.
FT DOMAIN 89 97 Complementarity-determining-4.
FT DOMAIN 98 107 Framework-3.
FT DISULFID 23 88 Framework-4.
FT NON_TER 108
SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;

Query Match      100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 71 FTLTISS 77

RESULT 9
KV1G_HUMAN
ID KV1G_HUMAN STANDARD; PRT; 108 AA.
AC P01599;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region Gal.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
```

RX MEDLINE=75059122; PubMed=4215718;
RA Laure C.J., Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT kappa-type, subgroup I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
CC macroglobulin.
DR PIR; A01867; KIHUGL.
DR HSSP; P01607; 1BWV.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FF73 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 71 FTLTISS 77

RESULT 10
KV1H HUMAN STANDARD; PRT; 108 AA.
ID -KV1H HUMAN
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01868; KIHUHU.
DR PDB; 1F6L; X-ray; L=1-108.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;

KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 71 FTLTISS 77

RESULT 11
KV1S HUMAN STANDARD; PRT; 108 AA.
ID -KV1S HUMAN
AC P01611;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region Wes.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81092279; PubMed=6778806;
RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolysate of a protein by
RT high-pressure liquid chromatography. The primary structure of a
RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein Wes).";
RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01877; KIHUWS.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 71 FTLTISS 77

```
RESULT 12
KV5Q_MOUSE
ID KV5Q_MOUSE STANDARD; PRT; 108 AA.
AC P01650;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region UPC 61.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79195288; PubMed=109517;
RA Vrana M., Rudikoff S., Potter M.;
RT "The structural basis of a haptin-inhibitable kappa-chain idiotype.";
RL J. Immunol. 122:1905-1910(1979).
CC -!- MISCELLANEOUS: This chain was isolated from myeloma proteins that
CC bind beta(2-1)-fructofuranosyl moieties (inulin).
DR PIR; A92808; KWS61.
DR HSSP; P01607; 1BWV.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON_TER 108
FT SEQUENCE 108 AA; 11809 MW; FAE4DA36076F2AFE CRC64;
Query Match
Best Local Similarity 100.0%; Score 32; DB 1; Length 108;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 71 FTLTISS 77

RESULT 13
KV5R_MOUSE
ID KV5R_MOUSE STANDARD; PRT; 108 AA.
AC P01651;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region EPC 109.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79195288; PubMed=109517;
RA Vrana M., Rudikoff S., Potter M.;
RT "The structural basis of a haptin-inhibitable kappa-chain idiotype.";
RL J. Immunol. 122:1905-1910(1979).
CC -!- MISCELLANEOUS: This chain was isolated from myeloma proteins that
CC bind beta(2-1)-fructofuranosyl moieties (inulin).
DR PIR; B92808; KWS609.
DR HSSP; P01607; 1BWV.
DR InterPro; IPR007110; Ig-like.
Query Match
Best Local Similarity 100.0%; Score 32; DB 1; Length 108;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 71 FTLTISS 77
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```
InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON_TER 108
FT SEQUENCE 108 AA; 11876 MW; 35C116BD60F79310 CRC64;
Query Match
Best Local Similarity 100.0%; Score 32; DB 1; Length 108;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 71 FTLTISS 77

RESULT 14
KV5S_MOUSE
ID KV5S_MOUSE STANDARD; PRT; 108 AA.
AC P01652;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region J606.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82099361; PubMed=6798111;
RA Johnson N., Slankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
RT binding proteins.";
RL J. Immunol. 128:302-307(1982).
CC -!- MISCELLANEOUS: This chain was isolated from myeloma proteins that
CC bind beta(2-1)-fructofuranosyl moieties (inulin).
DR PIR; A92811; KWS06.
DR HSSP; P01607; 1BWV.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON_TER 108
FT SEQUENCE 108 AA; 11810 MW; 8DE4DD31076F2AFB CRC64;
Query Match
Best Local Similarity 100.0%; Score 32; DB 1; Length 108;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 71 FTLTISS 77
```

```
RESULT 15
KVST_MOUSE
ID KVST_MOUSE STANDARD; PRT; 108 AA.
AC P01653;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region W3082.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82099361; PubMed=6798111;
RA Johnson N., Slankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
binding proteins.";
RL J. Immunol. 128:302-307(1982).
CC -!- MISCELLANEOUS: This chain was isolated from myeloma proteins that
bind beta(2-1)-fructofuranosyl moieties (inulin).
DR PIR; B92811; KMS82.
DR HSSP; P01607; IBWW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11850 MW; C5C145DC376F30CD CRC64;

Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
Db 71 FTLTSS 77
```

Search completed: November 4, 2004, 00:53:55
Job time : 104 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:33:03 ; Search time 60 Seconds
(without alignments)
41.852 Million cell updates/sec

Title: US-09-712-819D-1
Perfect score: 32
Sequence: 1 FTLTSS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	32	100.0	13	5	ADG67499 Humanised
2	32	100.0	13	5	ADG67501 Humanised
3	32	100.0	13	5	ADG67500 Humanised
4	32	100.0	13	5	ADG67502 Humanised
5	32	100.0	19	6	AAR87043 Human COU
6	32	100.0	32	2	AAR87043 Human gro
7	32	100.0	32	2	AAY52745 Humanised
8	32	100.0	32	4	AAB98288 Anti-A33
9	32	100.0	32	4	AAB97666 A33 antig
10	32	100.0	32	4	AAB97668 A33 antig
11	32	100.0	32	4	ABG98287 Human ant
12	32	100.0	32	5	AAE19672 Human gro
13	32	100.0	32	5	ABP62658 Human imm
14	32	100.0	32	5	ABP62658 Human imm
15	32	100.0	32	5	ABP62673 Human imm
16	32	100.0	32	5	AAU70396 Human lig
17	32	100.0	32	5	AAU70408 Human lig
18	32	100.0	32	5	AAU70436 Mouse lig
19	32	100.0	32	5	AAO17650 Human FAP
20	32	100.0	32	5	ABO10698 Deimmunis
21	32	100.0	32	6	ABR44642 Murine J5
22	32	100.0	32	6	AAB98288 Anti-A33
23	32	100.0	32	6	AAB97666 A33 antig
24	32	100.0	32	7	ABO33922 Anti-GPI-
25	32	100.0	32	7	ABO33921 Anti-GPI-

26	32	100.0	32	7	ABO33924	Anti-GPI-
27	32	100.0	32	8	ADH17942	Human 15H
28	32	100.0	32	8	ADH17975	Human mod
29	32	100.0	32	8	ADH17983	Human rhu
30	32	100.0	36	7	ABW01925	Antibody
31	32	100.0	42	5	ABG98296	Antibody
32	32	100.0	42	5	ABG98294	Human ant
33	32	100.0	42	5	ABG98288	Human ant
34	32	100.0	42	5	ABG98290	Antibody
35	32	100.0	50	5	ABG30482	Human ant
36	32	100.0	70	7	ABG75305	Human sub
37	32	100.0	70	8	ABM79517	Human DPK
38	32	100.0	74	2	AAR62921	Human cyt
39	32	100.0	74	2	AAW62805	Amino aci
40	32	100.0	75	2	AAR62923	Human cyt
41	32	100.0	76	2	AAW80981	Variable
42	32	100.0	76	6	ABO04843	Human epi
43	32	100.0	79	8	ADL35149	CEA4-8A a
44	32	100.0	79	8	ADL35148	Humanised
45	32	100.0	80	6	ABO10701	Deimmunis

ALIGNMENTS

RESULT 1
ADG67499
ID ADG67499 standard; peptide; 13 AA.
XX
AC ADG67499;
XX
DT 11-MAR-2004 (first entry)
XX
DE Humanised anti-Tac antibody MHC class II binding peptide #61.
XX
KW human; mouse; T-cell epitope; major histocompatibility complex; MHC;
KW immunogenicity; MHC class II; antibody.
XX
OS Homo sapiens.
XX
PN WO200269232-A2.
XX
PD 06-SEP-2002.
XX
PF 18-FEB-2002; 2002WO-EP001688.
XX
PR 19-FEB-2001; 2001EP-00103954.
PR 08-MAR-2001; 2001EP-00105777.
PR 15-MAR-2001; 2001EP-00106536.
PR 15-MAR-2001; 2001EP-00106538.
PR 20-MAR-2001; 2001EP-00106899.
PR 20-MAR-2001; 2001EP-00107012.
PR 27-MAR-2001; 2001EP-00107568.
PR 25-APR-2001; 2001EP-00110220.
PR 30-MAY-2001; 2001EP-00113228.
PR 19-OCT-2001; 2001EP-00124965.
PR 12-NOV-2001; 2001EP-00126859.
XX
(MERE) MERCK PATENT GMBH.
XX
PI Carr FU, Carter G, Jones T, Williams S, Hamilton A;
XX
WPI; 2002-750424/81.
XX
Identifying potential T-cell epitope peptides within the amino acid
sequence of a biological molecule, useful for preparing a biological
molecule with reduced immunogenicity, comprises determining peptide
binding to MHC molecules.
XX
Example 20; Page 60; 85pp; English.
XX
The invention relates to a novel method for identifying one or more
potential T-cell epitope peptides within the amino acid sequence of a

CC biological molecule by determining the binding of the peptides to major
CC histocompatibility complex (MHC) molecules using in vitro or in silico
CC techniques or biological assays. The method of the invention is useful
CC for preparing a polypeptide, a protein, a fusion protein, an antibody or
CC their fragments with reduced immunogenicity. The potential T-cell epitope
CC peptide within the amino acid sequence of a parent immunogenically non-
CC modified biological molecule identified is useful for preparing a
CC desired biological activity, where the T-cell epitope is a 13mer peptide.
CC The present sequence is used in the exemplification of the invention.

XX Sequence 13 AA;

SQ Query Match 100.0%; Score 32; DB 5; Length 13;

Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7

Db 7 FTLTISS 13

RESULT 2

ADG67501

ID ADG67501 standard; peptide; 13 AA.

XX AC ADG67501;

XX DT 11-MAR-2004 (first entry)

XX DE Humanised anti-Tac antibody MHC class II binding peptide #63.

XX KW human; mouse; T-cell epitope; major histocompatibility complex; MHC;

XX KW immunogenicity; MHC class II; antibody.

XX OS Homo sapiens.

XX PN WO200269232-A2.

XX PD 06-SEP-2002.

XX PF 18-FEB-2002; 2002WO-EP001688.

XX PR 19-FEB-2001; 2001EP-00103954.

XX PR 08-MAR-2001; 2001EP-00105777.

XX PR 15-MAR-2001; 2001EP-00106536.

XX PR 15-MAR-2001; 2001EP-00106538.

XX PR 20-MAR-2001; 2001EP-00106899.

XX PR 27-MAR-2001; 2001EP-00107568.

XX PR 25-APR-2001; 2001EP-00110220.

XX PR 30-MAY-2001; 2001EP-00113228.

XX PR 19-OCT-2001; 2001EP-00124965.

XX PR 12-NOV-2001; 2001EP-00126859.

XX PA (MERE) MERCK PATENT GMBH.

XX PI Carr FJ, Carter G, Jones T, Williams S, Hamilton A;

XX DR WPI; 2002-750424/81.

XX PT Identifying potential T-cell epitope peptides within the amino acid

XX PT sequence of a biological molecule, useful for preparing a biological

XX PT molecule with reduced immunogenicity, comprises determining peptide

XX PT binding to MHC molecules.

XX PS Example 20; Page 60; 85pp; English.

XX CC The invention relates to a novel method for identifying one or more

XX CC potential T-cell epitope peptides within the amino acid sequence of a

XX CC biological molecule by determining the binding of the peptides to major

XX CC histocompatibility complex (MHC) molecules using in vitro or in silico

XX CC techniques or biological assays. The method of the invention is useful

XX CC for preparing a polypeptide, a protein, a fusion protein, an antibody or

XX CC their fragments with reduced immunogenicity. The potential T-cell epitope

XX CC peptide within the amino acid sequence of a parent immunogenically non-

CC for preparing a polypeptide, a protein, a fusion protein, an antibody or
CC their fragments with reduced immunogenicity. The potential T-cell epitope
CC peptide within the amino acid sequence of a parent immunogenically non-
CC modified biological molecule identified is useful for preparing a
CC biological molecule with reduced immunogenicity and having a retained
CC desired biological activity, where the T-cell epitope is a 13mer peptide.
CC The present sequence is used in the exemplification of the invention.

XX SQ Sequence 13 AA;

Query Match 100.0%; Score 32; DB 5; Length 13;

Best Local Similarity 100.0%; Pred. No. 3.3;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7

Db 3 FTLTISS 9

RESULT 3

ADG67500

ID ADG67500 standard; peptide; 13 AA.

XX AC ADG67500;

XX DT 11-MAR-2004 (first entry)

XX DE Humanised anti-Tac antibody MHC class II binding peptide #62.

XX KW human; mouse; T-cell epitope; major histocompatibility complex; MHC;

XX KW immunogenicity; MHC class II; antibody.

XX OS Homo sapiens.

XX PN WO200269232-A2.

XX PD 06-SEP-2002.

XX PF 18-FEB-2002; 2002WO-EP001688.

XX PR 19-FEB-2001; 2001EP-00103954.

XX PR 08-MAR-2001; 2001EP-00105777.

XX PR 15-MAR-2001; 2001EP-00106536.

XX PR 15-MAR-2001; 2001EP-00106538.

XX PR 20-MAR-2001; 2001EP-00107012.

XX PR 27-MAR-2001; 2001EP-00107568.

XX PR 25-APR-2001; 2001EP-00110220.

XX PR 30-MAY-2001; 2001EP-00113228.

XX PR 19-OCT-2001; 2001EP-00124965.

XX PR 12-NOV-2001; 2001EP-00126859.

XX PA (MERE) MERCK PATENT GMBH.

XX PI Carr FJ, Carter G, Jones T, Williams S, Hamilton A;

XX DR WPI; 2002-750424/81.

XX PT Identifying potential T-cell epitope peptides within the amino acid

XX PT sequence of a biological molecule, useful for preparing a biological

XX PT molecule with reduced immunogenicity, comprises determining peptide

XX PT binding to MHC molecules.

XX PS Example 20; Page 60; 85pp; English.

XX CC The invention relates to a novel method for identifying one or more

XX CC potential T-cell epitope peptides within the amino acid sequence of a

XX CC biological molecule by determining the binding of the peptides to major

XX CC histocompatibility complex (MHC) molecules using in vitro or in silico

XX CC techniques or biological assays. The method of the invention is useful

XX CC for preparing a polypeptide, a protein, a fusion protein, an antibody or

XX CC their fragments with reduced immunogenicity. The potential T-cell epitope

XX CC peptide within the amino acid sequence of a parent immunogenically non-

CC modified biological molecule identified is useful for preparing a
 CC biological molecule with reduced immunogenicity and having a retained
 CC desired biological activity, where the T-cell epitope is a 13mer peptide.
 CC The present sequence is used in the exemplification of the invention.

XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 32; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
 Db 4 FTLTISS 10

RESULT 4
 ADG67502
 ID ADG67502 standard; peptide; 13 AA.
 XX
 AC ADG67502;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Humanised anti-Tac antibody MHC class II binding peptide #64.
 XX
 KW human; mouse; T-cell epitope; major histocompatibility complex; MHC;
 KW immunogenicity; MHC class II; antibody.
 XX
 OS Homo sapiens.
 XX
 PN WO200269232-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 18-FEB-2002; 2002WO-EP001688.
 XX
 PR 19-FEB-2001; 2001EP-00103954.
 PR 08-MAR-2001; 2001EP-00105777.
 PR 15-MAR-2001; 2001EP-00106536.
 PR 15-MAR-2001; 2001EP-00106538.
 PR 20-MAR-2001; 2001EP-00106899.
 PR 20-MAR-2001; 2001EP-00107012.
 PR 27-MAR-2001; 2001EP-00107568.
 PR 25-APR-2001; 2001EP-00110220.
 PR 30-MAY-2001; 2001EP-00113228.
 PR 19-OCT-2001; 2001EP-00124965.
 PR 12-NOV-2001; 2001EP-00126859.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Carr FJ, Carter G, Jones T, Williams S, Hamilton A;
 XX
 DR WPI; 2002-750424/81.
 XX
 PT Identifying potential T-cell epitope peptides within the amino acid
 PT sequence of a biological molecule, useful for preparing a biological
 PT molecule with reduced immunogenicity, comprises determining peptide
 PT binding to MHC molecules.

PS Example 20; Page 60; 85pp; English.
 XX
 CC The invention relates to a novel method for identifying one or more
 CC potential T-cell epitope peptides within the amino acid sequence of a
 CC biological molecule by determining the binding of the peptides to major
 CC histocompatibility complex (MHC) molecules using in vitro or in silico
 CC techniques or biological assays. The method of the invention is useful
 CC for preparing a polypeptide, a protein, a fusion protein, an antibody or
 CC their fragments with reduced immunogenicity. The potential T-cell epitope
 CC peptide within the amino acid sequence of a parent immunogenically non-
 CC modified biological molecule identified is useful for preparing a
 CC biological molecule with reduced immunogenicity and having a retained
 CC desired biological activity, where the T-cell epitope is a 13mer peptide.

CC The present sequence is used in the exemplification of the invention.
 XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 32; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
 Db 1 FTLTISS 7

RESULT 5
 AAE38112
 ID AAE38112 standard; peptide; 19 AA.
 XX
 AC AAE38112;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human COU-1 antibody VL FR3 peptide #4.
 XX
 KW Human; cancer-associated epitope; cytokeratin K8; cytokeratin K18; VL;
 KW adenocarcinoma; therapy; cancer; antibody; light chain variable region;
 KW framework region; FR.
 XX
 OS Homo sapiens.
 XX
 PN WO2003057168-A2.
 XX
 PD 17-JUL-2003.
 XX
 PF 03-JAN-2003; 2003WO-US000297.
 XX
 PR 03-JAN-2002; 2002US-0345208P.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Ditzel H, Jensenius JC;
 XX
 DR WPI; 2003-598315/56.
 XX
 PT Novel isolated cancer-associated epitope comprising two separate
 PT polypeptides, a cytokeratin 8 polypeptide and a cytokeratin 18
 PT polypeptide, useful as component of vaccine for preventing or treating
 PT adenocarcinoma.

PS Claim 15; Page 37; 155pp; English.
 XX
 CC The invention provides a cancer-associated epitope comprising two
 CC separate polypeptides, a cytokeratin 8 polypeptide and a cytokeratin 18
 CC polypeptide. Vaccine composition of the invention is useful for treating
 CC or preventing colon adenocarcinoma, ovarian adenocarcinoma, renal
 CC adenocarcinoma, mammary adenocarcinoma, lung adenocarcinoma, pancreatic
 CC adenocarcinoma or non-seminoma testis carcinoma. The invention is also
 CC useful for preparing a medicament for treating or preventing cancer in a
 CC mammal. The present sequence is human COU-1 cancer-associated epitope
 CC antibody VL (light chain variable region) FR (framework region) peptide

SQ Sequence 19 AA;
 Query Match 100.0%; Score 32; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
 Db 2 FTLTISS 8

RESULT 6
 AAR87043

ID AAR87043 standard; peptide; 32 AA.
XX
AC AAR87043;
XX
XX
DT 25-JUN-1996 (first entry)
XX
XX Human group I light chain framework 3.
DE
XX
KW Humanised antibody; interleukin-5; IL-5; recombinant antibody;
KW antibody engineering; monoclonal antibody; MAb; 39D10; CDR;
KW complementarity determining region; light chain; framework; eosinophilia;
KW allergy; asthma.
XX
OS Homo sapiens.
XX
XX WO9535375-A1.
PN
XX
PD 28-DEC-1995.
XX
XX
PF 16-JUN-1995; 95WO-GB001411.
XX
PR 17-JUN-1994; 94GB-00012230.
XX
XX (CLLT) CELLTech THERAPEUTICS LTD.
PA
XX
PI Emtage JS, Bodmer MW, Athwal DS;
XX
XX WPI; 1996-058412/06.
DR
XX
XX Anti-human IL-5 recombinant antibody - useful for preventing or reducing
PT eosinophilia and for treating certain allergic diseases, esp. asthma.
XX
XX Example 3; Fig 3; 69pp; English.
PS
XX
XX Framework regions (AAR87041-44) of human group I (gpl) germ line antibody
CC light chain showed homology to corresponding regions (AAR87045-48,
CC respectively) of the rat anti-human interleukin-5 monoclonal antibody
CC 39D10 light chain (see AAR87040). This homology was utilised in the
CC prodn. of a humanised 39D10 VL (AAR87057) in which rat 39D10 VL
CC complementarity determining regions were grafted into the human gpl
CC framework
XX
XX Sequence 32 AA;
SQ
Query Match 100.0%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLTISS 7
Db 15 FTLTISS 21
RESULT 7
AAY52745
ID AAY52745 standard; peptide; 32 AA.
XX
XX
AC AAY52745;
XX
XX
DT 26-JAN-2000 (first entry)
XX
XX Humanised ATR-5 L chain V region FR3 for a.
DE
XX
KW Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
KW ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
KW disseminated intravascular coagulation; immunogenicity; chimeric.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9951743-A1.
PN
XX
PD 14-OCT-1999.

XX 02-APR-1999; 99WO-JP001768.
PF
XX
PR 03-APR-1998; 98JP-00091850.
XX
XX (CHUS) CHUGAI SEIYAKU KK.
PA
XX
XX Sato K, Adachi H, Yabuta N;
PI
XX
DR WPI; 1999-620204/53.
XX
XX Humanised antibody recognizing human tissue factor, used for treatment of
PT disseminated intravascular coagulation.
XX
XX Claim 17; Page 270; 291pp; Japanese.
XX
XX The present invention describes chimeric antibody (Ab) heavy (H) chains
CC containing the variable region of the H chain of a mouse monoclonal Ab
CC recognising human tissue factor (htf) and the constant region of the H
CC chain of a human Ab. The variable region is one of six specified
CC sequences (which are the H chain variable regions from mouse monoclonal
CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L) chains
CC containing the variable region of the L chain of a mouse monoclonal Ab
CC recognising human tissue factor (htf) and the constant region of the L
CC chain of a human Ab, the variable region being one of six specified
CC sequences (which are the L chain variable regions from mouse monoclonal
CC Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for the treatment
CC and prevention of thrombotic disease, especially of disseminated
CC intravascular coagulation (DIC). The humanised antibody has the high htf
CC binding activity of the mouse monoclonal antibody but greatly reduced
CC immunogenicity. AAZ33001 to AAZ33091 and Y527007 to AAY52767 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 32 AA;
Query Match 100.0%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLTISS 7
Db 15 FTLTISS 21
RESULT 8
AAB98286
ID AAB98286 standard; peptide; 32 AA.
XX
XX
AC AAB98286;
XX
XX
DT 20-AUG-2001 (first entry)
XX
XX
DE Anti-A33 antigen immunoglobulin VL FR3 SEQ ID NO:92.
XX
XX Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
KW immunoglobulin; complementarity determining region; CDR; cancer;
KW cytostatic; anticancer; colon cancer; stomach cancer.
XX
XX Homo sapiens.
OS
XX WO200130393-A2.
PN
XX
XX 03-MAY-2001.
PD
XX
XX 20-OCT-2000; 2000WO-US029289.
PF
XX
XX 22-OCT-1999; 99US-00425638.
PR
XX 04-APR-2000; 2000US-00543004.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX (SCRI) SCRIPPS RES INST.
XX

PI Barbas CF, Rader C, Ritter G, Welt S, Old LJ;
 XX WPI; 2001-328613/34.
 XX
 PT Treating cancers, particularly of stomach and colon, that express A33
 PT antigen by administering conjugate of anticancer agent with specific
 PT immunoglobulin product.
 XX
 PS Claim 16; Page 40; 85pp; English.
 XX
 CC The present invention describes a method for treating cancers that
 CC express the A33 antigen. The method comprises administering an anticancer
 CC agent (I) conjugated to an immunoglobulin product (II) that binds
 CC specifically to A33 and contains one or more of 13 specified
 CC complementarity determining regions (CDRs), given in AAB98262 to
 CC AAB98274. (I) has cytostatic activity. The method can be used for
 CC treating colon and stomach cancers. (II), or the nucleic acid encoding
 CC it, can be used directly, in unconjugated form, for immunotherapy of
 CC cancer, and, when labeled, for detection or diagnosis of diseases
 CC associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to
 CC AAB98321 represent sequences used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 32 AA;
 Query Match 100.0%; Score 32; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTLTISS 7
 Db |||||
 15 FTLTISS 21
 RESULT 9
 AAB98288
 ID AAB98288 standard; peptide; 32 AA.
 XX
 AC AAB98288;
 XX
 DT 20-AUG-2001 (first entry)
 XX
 DE Anti-A33 antigen immunoglobulin VL FR3 SEQ ID NO:94.
 XX
 KW Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
 KW immunoglobulin; complementarity determining region; CDR; cancer;
 KW cytostatic; anticancer; colon cancer; stomach cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200130393-A2.
 XX
 PD 03-MAY-2001.
 XX
 PF 20-OCT-2000; 2000WO-US029289.
 XX
 PR 22-OCT-1999; 99US-00425638.
 PR 04-APR-2000; 2000US-00543004.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Barbas CF, Rader C, Ritter G, Welt S, Old LJ;
 XX WPI; 2001-328613/34.
 XX
 PT Treating cancers, particularly of stomach and colon, that express A33
 PT antigen by administering conjugate of anticancer agent with specific
 PT immunoglobulin product.
 XX
 PS Claim 16; Page 40; 85pp; English.
 XX

CC The present invention describes a method for treating cancers that
 CC express the A33 antigen. The method comprises administering an anticancer
 CC agent (I) conjugated to an immunoglobulin product (II) that binds
 CC specifically to A33 and contains one or more of 13 specified
 CC complementarity determining regions (CDRs), given in AAB98262 to
 CC AAB98274. (I) has cytostatic activity. The method can be used for
 CC treating colon and stomach cancers. (II), or the nucleic acid encoding
 CC it, can be used directly, in unconjugated form, for immunotherapy of
 CC cancer, and, when labeled, for detection or diagnosis of diseases
 CC associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to
 CC AAB98321 represent sequences used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 32 AA;
 Query Match 100.0%; Score 32; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTLTISS 7
 Db |||||
 15 FTLTISS 21
 RESULT 10
 AAB97666
 ID AAB97666 standard; peptide; 32 AA.
 XX
 AC AAB97666;
 XX
 DT 08-AUG-2001 (first entry)
 XX
 DE A33 antigen binding immunoglobulin product VLFR3 peptide SEQ ID NO:92.
 XX
 KW Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
 KW immunoreact; anti A33 antigen antibody; immunoglobulin.
 XX
 OS Homo sapiens.
 XX
 PN WO200131065-A1.
 XX
 PD 03-MAY-2001.
 XX
 PF 20-OCT-2000; 2000WO-US029026.
 XX
 PR 22-OCT-1999; 99US-00425638.
 PR 04-APR-2000; 2000US-00543004.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Barbas CF, Rader C;
 XX WPI; 2001-328657/34.
 XX
 PT Preparing humanized rabbit antibodies that specifically immunoreact with
 PT a particular antigen using display technology for expressing libraries of
 PT antibody domains and fine tuning variable domain regions.
 XX
 PS Example 9; Page 39; 62pp; English.
 XX
 CC The present invention describes a method for preparing a humanised rabbit
 CC antibody that specifically immunoreacts with a particular antigen. The
 CC method comprises expressing a library of antibodies comprising one or
 CC more complementarity determining region (CDR) from the variable domain
 CC sequences that specifically immunoreact with the antigen grafted into
 CC framework regions from humans, and selecting the antibodies that react
 CC with the antigen. The method is useful for humanising non-human mammalian
 CC antibodies, which can be used for the treatment of a variety of diseases.
 CC The present sequence represents an A33 antigen binding immunoglobulin
 CC product VLFR3 peptide which is given in an example from the present
 CC invention
 XX
 SQ Sequence 32 AA;

Query Match 100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 15 FTLTISS 21

RESULT 11

AAB97668
ID AAB97668 standard; peptide; 32 AA.

XX AC

XX AC AAB97668;

DT 08-AUG-2001 (first entry)

XX DE A33 antigen binding immunoglobulin product VLFR3 peptide SEQ ID NO:94.

XX KW Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
KW immunoreact; anti A33 antigen antibody; immunoglobulin.

XX OS Homo sapiens.

XX PN WO200131065-A1.

XX PD 03-MAY-2001.

XX PF 20-OCT-2000; 2000WO-US029026.

XX PR 22-OCT-1999; 99US-00425638.

XX PR 04-APR-2000; 2000US-00543004.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Barbas CF, Rader C;

XX DR WPI; 2001-328657/34.

XX PT Preparing humanized rabbit antibodies that specifically immunoreact with
PT a particular antigen using display technology for expressing libraries of
PT antibody domains and fine tuning variable domain regions.

PS Example 9; Page 39; 62pp; English.

XX CC The present invention describes a method for preparing a humanised rabbit
CC antibody that specifically immunoreacts with a particular antigen. The
CC method comprises expressing a library of antibodies comprising one or
CC more complementarity determining region (CDR) from the variable domain
CC sequences that specifically immunoreact with the antigen grafted into
CC framework regions from humans, and selecting the antibodies that react
CC with the antigen. The method is useful for humanising non-human mammalian
CC antibodies, which can be used for the treatment of a variety of diseases.
CC The present sequence represents an A33 antigen binding immunoglobulin
CC product VLFR3 peptide which is given in an example from the present
CC invention

XX SQ Sequence 32 AA;

Query Match 100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 15 FTLTISS 21

RESULT 12

ABG98287
ID ABG98287 standard; peptide; 32 AA.

XX

AC ABG98287;
XX 08-JAN-2003 (first entry)
DT Human antibody 012/V3b germline kappa chain variable region FR3/FR4 #1.
XX
DE XX
XX KW Antibody; variable region; light chain; heavy chain; VH; VL; gp39; CD40;
KW T-cell activation; B-cell differentiation; framework region;
KW cellular immune response; gene therapy; graft rejection; human; FR;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; diabetes;
KW asthma; multiple sclerosis; allergy; diabetes mellitus;
KW systemic lupus erythematosus; graft-versus-host disease.
XX OS Homo sapiens.
XX PN WO200194586-A2.
XX PD 13-DEC-2001.
XX PF 06-JUN-2001; 2001WO-US018098.
XX PR 06-JUN-2000; 2000US-0209584P.
XX PA (IDEC-) IDEC PHARM CORP.
XX Anderson DR, Pan LZ, Hanna N, Rastetter WH, Kloetzer WS;
XX WPI; 2002-188261/24.
XX PT New antibodies binding to an epitope on gp39, useful for preventing graft
PT rejection, or for treating autoimmune diseases (e.g. diabetes, asthma or
PT multiple sclerosis), and non-autoimmune diseases (e.g. graft-versus-host
PT disease).
XX PS Disclosure; Page 46; 130pp; English.
XX CC The invention relates to an antibody which binds to an epitope on gp39,
CC is new, where the epitope is distinct from the epitope bound by IDEC-131,
CC and the antibody has a non-agonistic effect on T-cell activation and
CC inhibits gp39/CD40 interaction. Also included are: (1) an improved method
CC of treating a disease by modulating gp39 expression or inhibiting the
CC gp39/CD40 interaction comprising administering an antibody specific for
CC gp39 that inhibits the gp39/CD40 interaction and is non-agonistic of T-
CC cell activation; (2) an antibody which antagonises B-cell differentiation
CC and antibody production, and is non-agonistic of T-cell activation; (3)
CC a DNA sequence which encodes an antibody defined above; (4) an expression
CC vector, which contains a DNA sequence of (3); (5) a method of suppressing
CC humoral and/or cellular immune responses against cells or vectors
CC administered during cell or gene therapy comprising further administering
CC prior, during or after gene therapy, an antibody defined above; and (6)
CC an improved method of treatment which involves the transplantation of
CC cells, tissues or organs of the same or different species into a subject,
CC where the improvement comprises administering an antibody defined above
CC prior, during or after transplantation, to suppress immune responses
CC against the transplanted cell, tissue or organ, or to suppress immune
CC responses elicited by the transplanted cell, tissue or organ against the
CC host. The antibody is useful for preventing graft rejection, and for
CC treating autoimmune diseases, e.g., rheumatoid arthritis, multiple
CC sclerosis, diabetes, asthma, multiple sclerosis, allergic conditions,
CC diabetes mellitus, or systemic lupus erythematosus, as well as non-
CC autoimmune diseases such as graft-versus-host disease (many other
CC diseases and conditions are given in the specification). The antibodies
CC are also useful in gene or cellular therapy, and to inhibit humoral and
CC cellular immune responses against viral vectors. The present sequence is
CC a framework region (FR) fragment of a human anti-gp39 antibody used to
CC determine which amino acids should be humanised in a mouse anti-gp39
CC molecule
XX SQ Sequence 32 AA;

Query Match 100.0%; Score 32; DB 5; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	FTLTISS 7	
Db	15	FTLTISS 21	
RESULT 13			
AAE19672			
ID	AAE19672 standard; peptide; 32 AA.		
XX			
AC	AAE19672;		
XX			
DT	31-MAY-2002 (first entry)		
XX			
DE	Human group 1 consensus peptide #3.		
XX			
KW	Human; tumour necrosis factor 40; TNF40; osteopathic; cardiant; CDR;		
KW	complementarity determining region; rheumatoid; osteo-arthritis; sepsis;		
KW	congestive heart failure; shock; tissue transplant; tuberculosis; AIDS;		
KW	Acquired Immune Deficiency Syndrome; adult respiratory distress syndrome;		
KW	cachexia; allergy; psoriasis; blood coagulation disorder; thyroiditis;		
KW	inflammatory bone disorder; Crohn's disease; autoimmune disease; burn;		
KW	neoplasty therapy; immunomodulator; vulnery; graft rejection.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200194585-A1.		
XX			
PD	13-DEC-2001.		
XX			
PF	05-JUN-2001; 2001WO-GB002477.		
XX			
PR	06-JUN-2000; 2000GB-00013810.		
XX			
PA	(CELL-) CELLTECH R & D LTD.		
XX			
PI	Athwal DS, Brown DT, Weir ANC, Popplewell AG, Chapman AP;		
PI	King DJ;		
XX			
DR	WPI; 2002-216732/27.		
XX			
PT	New antibody specific for human tumor necrosis factor (TNF)-alpha, useful		
PT	for treating TNF-alpha-mediated diseases, e.g. congestive heart failure,		
PT	septic or endotoxic shock, cachexia, adult respiratory distress syndrome.		
XX			
PS	Example 1; Fig 1; 119pp; English.		
XX			
CC	The invention relates to an antibody molecule having specificity for		
CC	human tumour necrosis factor-alpha (TNFalpha) comprising a heavy or light		
CC	chain. The antibody or the compound comprising the antibody is useful for		
CC	treating or manufacturing a medicament for treating a pathology mediated		
CC	by TNFalpha, such as rheumatoid or osteo-arthritis. TNFalpha mediated		
CC	diseases which can be treated by the antibody include sepsis, congestive		
CC	heart failure, septic or endotoxic shock, cachexia, adult respiratory		
CC	distress syndrome, acquired immunodeficiency syndrome (AIDS), allergies,		
CC	psoriasis, tuberculosis, inflammatory bone disorders, blood coagulation		
CC	disorders, burns, rejection episodes following organ or tissue		
CC	transplant, Crohn's disease and autoimmune diseases, such as thyroiditis.		
CC	The antibodies may also be used to reduce the side effects associated		
CC	with TNFalpha generation during neoplasty therapy, to eliminate or reduce		
CC	shock-related symptoms associated with the treatment or prevention of		
CC	graft rejection by use of an anti-lymphocyte antibody, for treating multi		
CC	-organ failure, or in the diagnosis and imaging of disease states		
CC	involving elevated levels of TNF alpha. The present sequence is human		
CC	group 1 consensus peptide used in the exemplification of the invention		
XX			
SQ	Sequence 32 AA;		
Query Match 100.0%; Score 32; DB 5; Length 32;			
Best Local Similarity 100.0%; Pred. No. 8.9;			
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	FTLTISS 7	

Db	15	FTLTISS 21	
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ID	ABP62658 standard; peptide; 32 AA.		
XX			
AC	ABP62658;		
XX			
DT	10-OCT-2002 (first entry)		
XX			
DE	Human immunopeptide to HCV E2 glycoprotein framework sequence #166.		
XX			
KW	Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;		
KW	nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;		
KW	NS3 protein; viral infection.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200259340-A1.		
XX			
PD	01-AUG-2002.		
XX			
PF	25-JAN-2002; 2002WO-US002303.		
XX			
PR	26-JAN-2001; 2001US-0264451P.		
XX			
PA	(SCRI) SCRIPPS RES INST.		
XX			
PI	Maruyama T, Jones IM, Burton DR, Fox RI;		
XX			
DR	WPI; 2002-599801/64.		
XX			
PT	New human immunopolypeptide with binding specificity for certain envelope		
PT	glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for		
PT	diagnosing or treating patients having or suspected of having HCV		
PT	infection.		
XX			
PS	Claim 4; Fig 17; 308pp; English.		
XX			
CC	The present invention relates to human immunopolypeptides, produced by a		
CC	phage transfected cell library. The present sequence is one such		
CC	immunopolypeptide. The immunopolypeptides have binding specificity for		
CC	envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C		
CC	virus (HCV). E2 glycoprotein is believed to be responsible for target		
CC	cell binding and contains neutralising epitopes, while NS3 is thought to		
CC	be involved in the replication of HCV. The immunopolypeptides are useful		
CC	for diagnosing and treating a patient having or suspected to be having		
CC	HCV infection		
XX			
SQ	Sequence 32 AA;		
Query Match 100.0%; Score 32; DB 5; Length 32;			
Best Local Similarity 100.0%; Pred. No. 8.9;			
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	FTLTISS 7	
Db	15	FTLTISS 21	
RESULT 15			
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ID	ABP62688 standard; peptide; 32 AA.		
XX			
AC	ABP62688;		
XX			
DT	10-OCT-2002 (first entry)		
XX			
DE	Human immunopeptide to HCV E2 glycoprotein framework sequence #196.		
XX			
KW	Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;		

KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW NS3 protein; viral infection.
XX
OS Homo sapiens.
XX
PN WO200259340-A1.
XX
PD 01-AUG-2002.
XX
XX 25-JAN-2002; 2002WO-US002303.
PF
XX 26-JAN-2001; 2001US-0264451P.
PR
XX (SCRI) SCRIPPS RES INST.
PA
XX Maruyama T, Jones IM, Burton DR, Fox RI;
PI
XX WPI; 2002-599801/64.
DR
XX New human immunopolypeptide with binding specificity for certain envelope
PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
PT diagnosing or treating patients having or suspected of having HCV
PT infection.
PT
XX
PS Claim 4; Fig 17; 308pp; English.
XX
CC The present invention relates to human immunopolypeptides, produced by a
CC phage transfected cell library. The present sequence is one such
CC immunopolypeptide. The immunopolypeptides have binding specificity for
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC virus (HCV). E2 glycoprotein is believed to be responsible for target
CC cell binding and contains neutralising epitopes, while NS3 is thought to
CC be involved in the replication of HCV. The immunopolypeptides are useful
CC for diagnosing and treating a patient having or suspected to be having
CC HCV infection
XX
SQ Sequence 32 AA;
Query Match 100.0%; Score 32; DB 5; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLTISS 7
Db 15 FTLTISS 21

Search completed: November 4, 2004, 00:47:39
Job time : 62.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:48:50 ; Search time 72.3333 Seconds
(without alignments)
31.376 Million cell updates/sec

Title: US-09-712-819D-1
Perfect score: 32
Sequence: 1 FTLTISS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	32	100.0	13	16	US-10-468-496-1991
2	32	100.0	13	16	US-10-468-496-1992
3	32	100.0	13	16	US-10-468-496-1993
4	32	100.0	13	16	US-10-468-496-1994
5	32	100.0	32	9	US-09-855-271-13
6	32	100.0	32	9	US-09-828-708-95
7	32	100.0	32	9	US-09-828-708-96
8	32	100.0	32	9	US-09-828-708-98
9	32	100.0	32	9	US-09-949-559-91
10	32	100.0	32	10	US-09-874-141-15
11	32	100.0	32	10	US-09-875-221A-91
12	32	100.0	32	10	US-09-563-222-76
13	32	100.0	32	10	US-09-563-222-88

14	32	100.0	32	10	US-09-563-222-116	Sequence 116, Appl
15	32	100.0	32	10	US-09-791-551-35	Sequence 35, Appl
16	32	100.0	32	14	US-10-160-506-15	Sequence 15, Appl
17	32	100.0	32	15	US-10-449-566-87	Sequence 87, Appl
18	32	100.0	32	15	US-10-443-466A-51	Sequence 51, Appl
19	32	100.0	32	15	US-10-443-466A-84	Sequence 84, Appl
20	32	100.0	32	15	US-10-443-466A-92	Sequence 92, Appl
21	32	100.0	32	15	US-10-462-062-129	Sequence 129, Appl
22	32	100.0	32	16	US-10-449-379-15	Sequence 15, Appl
23	32	100.0	32	16	US-10-688-015-15	Sequence 15, Appl
24	32	100.0	32	16	US-10-632-706-248	Sequence 248, Appl
25	32	100.0	32	16	US-10-632-706-251	Sequence 251, Appl
26	32	100.0	32	16	US-10-632-706-254	Sequence 254, Appl
27	32	100.0	32	16	US-10-632-706-257	Sequence 257, Appl
28	32	100.0	32	16	US-10-632-706-260	Sequence 260, Appl
29	32	100.0	32	16	US-10-632-706-263	Sequence 263, Appl
30	32	100.0	32	16	US-10-632-706-266	Sequence 266, Appl
31	32	100.0	32	16	US-10-632-706-269	Sequence 269, Appl
32	32	100.0	32	16	US-10-632-706-272	Sequence 272, Appl
33	32	100.0	32	16	US-10-632-706-275	Sequence 275, Appl
34	32	100.0	32	17	US-10-783-950-76	Sequence 76, Appl
35	32	100.0	32	17	US-10-783-950-86	Sequence 86, Appl
36	32	100.0	32	17	US-10-783-950-110	Sequence 110, Appl
37	32	100.0	36	14	US-10-387-645-5	Sequence 5, Appl
38	32	100.0	42	10	US-09-874-141-16	Sequence 16, Appl
39	32	100.0	42	10	US-09-874-141-18	Sequence 18, Appl
40	32	100.0	42	10	US-09-874-141-22	Sequence 22, Appl
41	32	100.0	42	10	US-09-874-141-24	Sequence 24, Appl
42	32	100.0	70	14	US-10-171-681-9	Sequence 9, Appl
43	32	100.0	70	14	US-10-171-680-9	Sequence 9, Appl
44	32	100.0	70	14	US-10-428-408A-17	Sequence 17, Appl
45	32	100.0	70	15	US-10-428-894-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1

US-10-468-496-1991
; Sequence 1991, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1991
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope

US-10-468-496-1991

Query Match 100.0%; Score 32; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTISS 7
|||||||
Db 7 FTLTISS 13

RESULT 2

US-10-468-496-1992
; Sequence 1992, Application US/10468496
; Publication No. US20040180386A1

; GENERAL INFORMATION:

; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita

; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL

; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED

; TITLE OF INVENTION: IMMUNOGENICITY

; FILE REFERENCE: MER-117

; CURRENT APPLICATION NUMBER: US/10/468,496

; CURRENT FILING DATE: 2003-09-25

; PRIOR APPLICATION NUMBER: 01103954.2

; PRIOR FILING DATE: 2001-02-19

; PRIOR APPLICATION NUMBER: 01105777.5

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: 01106538.0

; PRIOR FILING DATE: 2001-03-15

; PRIOR APPLICATION NUMBER: 01106536.4

; PRIOR FILING DATE: 2001-03-15

; PRIOR APPLICATION NUMBER: 01107012.5

; PRIOR FILING DATE: 2001-03-20

; PRIOR APPLICATION NUMBER: 01106899.6

; PRIOR FILING DATE: 2001-03-20

; NUMBER OF SEQ ID NOS: 2036

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1992

; LENGTH: 13

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: MHC class II binding epitope

US-10-468-496-1992

Query Match

Best Local Similarity 100.0%; Score 32; DB 16; Length 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTISS 7
|||||||
Db 4 FTLTISS 10

RESULT 3

US-10-468-496-1993

; Sequence 1993, Application US/10468496

; Publication No. US20040180386A1

; GENERAL INFORMATION:

; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita

; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL

; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED

; TITLE OF INVENTION: IMMUNOGENICITY

; FILE REFERENCE: MER-117

; CURRENT APPLICATION NUMBER: US/10/468,496

; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1993
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-1993

Query Match

Best Local Similarity 100.0%; Score 32; DB 16; Length 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTISS 7
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Db 3 FTLTISS 9

RESULT 4

US-10-468-496-1994

; Sequence 1994, Application US/10468496

; Publication No. US20040180386A1

; GENERAL INFORMATION:

; APPLICANT: Carr, Francis J.

; APPLICANT: Carter, Graham

; APPLICANT: Jones, Tim

; APPLICANT: Williams, Stephen

; APPLICANT: Hamilton, Anita

; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL

; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED

; TITLE OF INVENTION: IMMUNOGENICITY

; FILE REFERENCE: MER-117

; CURRENT APPLICATION NUMBER: US/10/468,496

; CURRENT FILING DATE: 2003-09-25

; PRIOR APPLICATION NUMBER: 01103954.2

; PRIOR FILING DATE: 2001-02-19

; PRIOR APPLICATION NUMBER: 01105777.5

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: 01106538.0

; PRIOR FILING DATE: 2001-03-15

; PRIOR APPLICATION NUMBER: 01106536.4

; PRIOR FILING DATE: 2001-03-15

; PRIOR APPLICATION NUMBER: 01107012.5

; PRIOR FILING DATE: 2001-03-20

; PRIOR APPLICATION NUMBER: 01106899.6

; PRIOR FILING DATE: 2001-03-20

; NUMBER OF SEQ ID NOS: 2036

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1994

; LENGTH: 13

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: MHC class II binding epitope

US-10-468-496-1994

Query Match

Best Local Similarity 100.0%; Score 32; DB 16; Length 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
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Db 1 FTLTISS 7

RESULT 5

US-09-855-271-13
; Sequence 13, Application US/09855271
; Patent No. US20020042089A1
; GENERAL INFORMATION:
; APPLICANT: Bodmer, Mark W
; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Emtage, John Spencer
; TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
; FILE REFERENCE: CARP-0088
; CURRENT APPLICATION NUMBER: US/09/855,271
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/347,061
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus
US-09-855-271-13

Query Match 100.0%; Score 32; DB 9; Length 32;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
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Db 15 FTLTISS 21

RESULT 6

US-09-828-708-95
; Sequence 95, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-95

Query Match 100.0%; Score 32; DB 9; Length 32;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
|||||||
Db 15 FTLTISS 21

RESULT 7

US-09-828-708-96
; Sequence 96, Application US/09828708
; Patent No. US20020146753A1

; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.

; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-96

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Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
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Db 15 FTLTISS 21

RESULT 8

US-09-828-708-98
; Sequence 98, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-98

Query Match 100.0%; Score 32; DB 9; Length 32;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
|||||||
Db 15 FTLTISS 21

RESULT 9

US-09-949-559-91
; Sequence 91, Application US/09949559
; Patent No. US20020151682A1
; GENERAL INFORMATION:
; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Brown, Derek Thomas
; APPLICANT: Weir, Andrew Neil Charles
; APPLICANT: Popplewell, Andrew George
; APPLICANT: Chapman, Andrew Paul
; APPLICANT: King, David John
; TITLE OF INVENTION: Biological Products
; FILE REFERENCE: Carp-0095
; CURRENT APPLICATION NUMBER: US/09/949,559
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 0013810.7GB
; PRIOR FILING DATE: 2000-06-06

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; PRIOR APPLICATION NUMBER: 09/875,221
; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human group 1
; US-09-949-559-91

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Query Match	100.0%;	Score 32;	DB 9;	Length 32;
Best Local Similarity	100.0%;	Pred. No. 16;		
Matches	7;	Conservative	0;	Mismatches 0; Indels

Qy	1	FTLTISS 7
pb	15	FTLTISS 21

RESULT 10

US-09-874-141-15
; Sequence 15, Application US/09874141
; Publication No. US20030012781A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL
; APPLICANT: PAN, LI-ZHEN
; APPLICANT: HANNA, NABIL
; APPLICANT: RASTETTER, WILLIAM H.
; APPLICANT: KLOETZER, WILLIAM S.
; TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS
; TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-0280632
; CURRENT APPLICATION NUMBER: US/09/874,141
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/209,584
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-874-141-15

Query Match	100.0%;	Score 32;	DB 10;	Length 32;
Best Local Similarity	100.0%;	Pred. No. 16;		
Matches	7: Conservative	0: Mismatches	0: Indels	0: Gaps

Qy	1	FTLTISS	7
Db	15	FTLTISS	21

RESULT 11
US-09-875-221A-91
; Sequence 91, Application US/09875221A
; Publication No. US20030026805A1
; GENERAL INFORMATION:
; APPLICANT: Atwal, Diljeet Singh
; APPLICANT: Brown, Derek Thomas
; APPLICANT: Weir, Andrew Neil Charles
; APPLICANT: Popplewell, Andrew George
; APPLICANT: Chapman, Andrew Paul
; APPLICANT: King, David John
; TITLE OF INVENTION: Biological Products
; FILE REFERENCE: Carp-0089
; CURRENT APPLICATION NUMBER: US/09/875,221A
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: GB0013810.7
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 130

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; SOFTWARE: PatentIn version 3.1.
; SEQ ID NO 91
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human group
US-09-875-221A-91

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Query Match	100.0%;	Score 32;	DB 10;	Length 32;
Best Local Similarity	100.0%;	Pred. No. 16;		
Matches	7: Conservative	0: Mismatches	0: Indels	

Qy	1	FTLTISS 7
pb	15	FTLTISS 21

RESULT 12

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US-09-563-222-76
; Sequence 76, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapien
;
US-09-563-222-76

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Query Match	100.0%;	Score 32;	DB 10;	Length 32;
Best Local Similarity	100.0%;	Pred. No. 16;		
Matches 7: Conservative	0;	Mismatches 0;	Indels	

Qy	1	FTLTISS 7
Db	15	FTLTISS 21

RESULT 13
US-09-563-222-88
; Sequence 88, Application US/09563222
; Publication No. US20030079253A1

Query Match	100.0%;	Score 32;	DB 10;	Length 32;
Best Local Similarity	100.0%;	Pred. No. 16;		
Matches	7;	Conservative	0;	Mismatches
				0;
				Indels
				0;

Qy 1 FTLTSS 7

Db 15 FTLTISS 21

RESULT 14
US-09-563-222-116
; Sequence 116, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 116
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-116

Query Match 100.0%; Score 32; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLTISS 7
Db 15 FTLTISS 21

RESULT 15
US-09-791-551-35
; Sequence 35, Application US/09791551
; Publication No. US20030235584A1
; GENERAL INFORMATION:
; APPLICANT: KLOETZER, WILLIAM S.
; APPLICANT: HANNA, NABIL
; TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
; FILE REFERENCE: 037003/0277869
; CURRENT APPLICATION NUMBER: US/09/791,551
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/185,390
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/233,625
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-791-551-35

Query Match 100.0%; Score 32; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLTISS 7
Db 15 FTLTISS 21

Search completed: November 4, 2004, 01:13:28
Job time : 73.3333 secs

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